GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2002, 10:04:11; Search time 33 Seconds (without alignments) 429.846 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-835-922-2 1778 1 MQAVDNLTSAPGNTSLCTRD.....SQDNRKKEQDGGDPNEETPM 342

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

imum DB seq length: 0 kimum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Query Match		BB	ID	Description
	0	342	۳ ا	P2YC_HUMAN	Q9h244 homo sapien
		342	۔ ــ	P2YC_MACFA	macac
	7.	347	H	P2YC_MOUSE	
	6	343	H	P2YC_RAT	Q9epx4 rattus norv
	•	338	L	P2YX_HUMAN	
•	•	338	1	P2YX_MOUSE	Bum
694		305	_	P2YX_RAT	035881 rattus norv
488	•	319	Ь	H963_HUMAN	
411.5	•	375	ب	GP34_MOUSE	
409.5	•	381	Ь	GP34_HUMAN	
394	•	342	_	PAFR_HUMAN	homo
392.5	•	342	₽	PAFR_CAVPO	6 cavia
٠.	•	361	_	EBI2_HUMAN	homo s
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n or		341	٠,	PAFR_MOUSE	Q62035 mus musculu
0		34 L	۰,	PAFK_KAT	rattus nor
		308	· -	P2Y5_CHICK	
	•	340	٠,	CLT2_HUMAN	homo sap
	•	537	-	P2Y8_XENLA	
4	•	309	_	CLT2_MOUSE	Q920a1 mus musculu
339.5		309	-	CLT2_RAT	Q924t9 rattus norv
339	٠	359	-	AG2R_BOVIN	P25104 bos taurus
338	٠	344	-	P2Y5_HUMAN	homo
334	•	359		AG2R_SHEEP	STAO
334	•	367	μ	GP17_HUMAN	homo
329	٠	359		AG2S_HUMAN	homo
328	•	340	Н	CLT1_PIG	s sns
327		359	Н	AG2R_PIG	
		359	\vdash	AG2R_CANFA	P43240 canis famil
N	•	399	٢	PAR2_MOUSE	
325	•	359	Н	AG2R_RABIT	P34976 oryctolagus
321	18.1	359	ب	AG2R_HUMAN	
920	18.0	359	Н	AG2R_CAVPO	Q9wv26 cavia porce
	Score 1778 1728.5 1528.5 1528.5 1528.5 1694 409.5 409.5 394.3 379.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5 347.5	Query Ref. 100.0 Ref. 100.0	Query Query Match Length 100.0 342 8 87.3 8 88.0 34.7 34.4 34.3 34.7 35.6 41.7 34.7 34.7 34.7 34.7 34.7 34.7 34.7 34	Query Ref. 100.0 Ref. 100.0	Query Query Hatch Length DB 100.0 342 1 58 87.5 88.0 342 1 58 88.0 342 1 343 338 1 344 1 338 1 345 2 20.4 341 1 342 1 344 1 34

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sequence. ";	waki S., Haga T., Takaesu H., Mitaku S.;	E FROM N.A.	[5]	TWEI /Corport /DOET databac	"ADP-glucose activates a G-protein coupled receptor and inhibits		Notherfor E. D. Berg 7 70mg T. Shlort F		Mol. Pharmacol. 60:432-439(2001).	receptor.";	ing of the platelet P2T(AC) ADP receptor:	., Soga T., Matsushime H., Furuichi K.;	Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto SI.,	281;	TISSTEERTAID:		Bio	SP1999.":	na F.J. Jr.;	Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,	Smith M	TISSUE=Hypothalamus;	SEQUENCE FROM N.A.		Nature 409:202-207(2001).	"Identification of the platefet ADP receptor targeted by		lshnan V., Yang RB., Nurden P., Nurden A., Julius	Hollopeter G., Jantzen HM., Vincent D., Li G., England L.,	SEQUENCE FROM N.A.		ritmuces, cacarrari,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Futboria: Drimatos: Catarrhini: Nominidae: Nomo).	P2RY12 OR HORK3.	(ADP-GIUCOSE receptor) (ADPG-K) (PZI(AC)) (PZI(CYC)) (PZI(AC)) (SP1999).	ptor 12 (P2Y12) (P2Y12 platele	(Rel. 41, Last annotation update)	15-JUN-2002 (Rel. 41, Lieated)	1001 11 0000000000000000000000000000000	PZYC_HUMAN STANDARD; PRT; 342 AA.	LHUMAN	

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FUNCTION: Receptor for ADP and ATP coupled to G-proteins that inhibit the adenylyl cyclase second messenger system. Not activated by UDP and UTP. Involved in platelets aggregation. SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Highly expressed in the platelets, lower levels in the brain. Lowest levels in the platelets, pluster levels in the datenal gland. Expressed in the spinal cord and the fetal brain.
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, AF321815; AAK00948.1; -.
; AB052684; BAB60824.1; -.
, AF310685; AAL32292.1; -.
; AB083596; BAB89309.1; -.
                  DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS
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DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS
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PR00237; GPCRRHODOPSN.
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7 58 CYTOPLASMIC (POTENTIAL).

9 9 EXTRACELLULAR (POTENTIAL).

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                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Frontal cortex, and Medulla oblongata; Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain
                                                                                                                                                                                                                                                                    EMBL; AB056385; BAB33041.1; -. EMBL; AB062981; BAB60747.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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JUN-2002 (Rel. 41, Last annotation update)
purinoceptor 12 (P2Y12).
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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ALIGNMENTS

RESULT 1 AAW81576 22-FEB-1999 AAW81576; AAW81576 standard; Protein; 342 AA. EBV-induced G-protein coupled receptor (EBI-2) polypeptide (first entry)

EBV-induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer; endothelium-differentlation gene; EDG-1-like G-protein coupled receptor; recombinant; agonist; asthma; Parkinson's disease; heart failure; asthma; hypotension; urinary retention; osteoporosis; antagonist; hypertension; angina pectoris; myocardial infarction; allergy; psychosis; depression; migraine; vomiting; stroke; eating disorder; migraine headache; cancer; prostatic hypertrophy; detection; drug screening.

Homo sapiens.

07-MAY-1998; Misc-difference Misc-difference 07-MAY-1997; WO9850549-A2 12-NOV-1998. 97US-0852824 98WO-US09048 Location/Qualifiers /note= /note= "encoded by AAC" "encoded by ATT"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide. The encoding DNA is deposited under the accession number ATC No: 209003. The invention provides two human G-protein coupled receptor polypeptides. The polypeptides are human Epstein-Barr Virus (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide and a human endothelium-differentiation gene (EBO) like G-protein coupled receptor, designated EBI-1 like G-protein coupled receptor. Vectors comprising the EBI-2 and EBG-1-like G-protein coupled receptor. Vectors comprising the EBI-2 and EBG-1-like polypeptides encoding DNA can be used to transform host cells for the recombinant production of the proteins. Agonists for G-protein coupled receptors can be used for the treatment of asthma, Parkinson's disease, acute heart failure, bypotension, urinary retention and osteoporosis. Antagonists can be used for the treatment of hypertension, angina pectoris, myocardial infarction, ulcers, asthma, allergies, psychoses, depression, migraine, vomiting, stroke, eating disorders, migraine headaches, cancer and benign prostatic hypertrophy. The products can also be used for detection, diagnosis and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                              AAY71306
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protein-coupled receptor hCHN8
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The present amino acid sequence is the hCHNB, an endogenous human corphan G protein-coupled receptor (GPCR), expressed in left and right cerebellum, kidney and lung. The hCHNB cDNA was identified using full length EST (expressed sequence tag) 764455 as a probe.

The orphan GPCR of the invention, like all GPCRs has seven transmembrane calpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR agonists and antagonists for use as pharmaceutical agents. The proteins can also be used in the study of GPCR-mediated signalling cascades, and to elucidate their precise role in normal and diseased human conditions. Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their protein in healthy and pathological states.
    Query Match
Best Local Similarity
Matches 342; Conserv
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26-FEB 1999
112-MAR-1999
112-MAR-1999
112-MAR-1999
28-MAY-1999
28-MAY-1999
28-MAY-1999
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28-MAY-1999
29-SEP-1999
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      Conservative
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990S-0137127
990S-0137121
990S-0156653
990S-0156633
990S-0156633
990S-0157280
990S-0157280
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99US-0416760.
99US-0417044.
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Score 1778; DB 21
Pred. No. 5e-187;
; Mismatches 0;
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RESULT 3
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27-NOV-1998;
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28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
28-MAY-1999;
30-JUN-1999;
30-JUN-1999;
27-AUG-1999;
03-SEP-1999;
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26-FEB-1999
12-MAR-1999
12-MAR-1999
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12-NOV-1998;
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                                                                                                                                                                                                                                                                                                                 Human; G protein coupled receptor; GPCR; transmembrane receptor;
identification; agonist; screening; therapeutic; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                        AAB02840 standard; Protein; 342
Behan DP, Lehmann-Bruinsma
Gore M, Liaw CW, Lin I, I
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                        (AREN-) ARENA PHARM INC
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99US-0121852

99US-0123944

99US-0123945

99US-0123948

99US-0123949

99US-0123949

99US-0123951

99US-0136437

99US-0136437

99US-0137127

99US-0137131

99US-0137131

99US-0137131

99US-0137131

99US-0137131

99US-0156533

99US-0156533
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98US-0108029.
98US-0109213.
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K, Chalmers DT,
Lowitz K, White
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                                                                                                             Human; G-protein-coupled receptor; GPCR; 15625 receptor protein; glial cells; spleen; colon; liver; brain; T-cell; heart; red cell; thymus; B-cell; pancreas; disorder; chromosome 3; anaemia; neutropenia; thrombocytopenia; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used the exemplification of the present invention.
  Misc-difference
                           Modified-site
                                                                                         Homo
                                                                                                                                                                             Human 15625
                                                                                                                                                                                                                                                    AAY94444 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 112-113; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-endogenous, human G protein-coupled receptors for screening receptor, inverse or partial agonists useful as therapeutic agents
                                                    Domain
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mes 342; Conserv
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                                                                                                                                                                             receptor
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 /label=
13
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6..9
                                                               Location/Qualifiers
                                                                                                                                                                            protein.
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                                       extracellular_domain
             N-glycosylation
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Pred. No. 5e-187;
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Best Local Similarity
                                                                                                                          Matches
                                                                                                                                                                                                                                                         The present sequence shows the 15625 receptor protein. It is a novel G-coupled protein receptor (GPCR). The CDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polynucleotides are useful for generating
                                                                                                                                                                                            The 15625 receptor protein polynical cotides are useful for generating probes, primers and antisense constructs. The polynical cotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be treated using the 15625 receptor protein polynical cotides and polypeptides include anaemia, neutropenia and thrombocytopenia.
                                                                                                                                                                                                                                                                                                                                                                                            Identifying an agent modulating the level or activity of G-protein coupled receptor useful for screening a cell derived from a subject having disorders such as anaemia, neutropenia and thrombocytopenia
                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glucksmann MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-1998;
25-AUG-1999;
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                                                                     DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS
                                                                                                                                                                         342 AA;
                                                                                                                          Conservative
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99US-0382918.
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173..176
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333..338
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13..16
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163..165
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                                                                                                                                    Score 1778; DB 2
Pred. No. 5e-187;
                                                                                                                        Mismatches
                                                                                                                                              DB 21;
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RESULT 5
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                      The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity tissue growth factor activity, immunomodulatory activity and activity in the diagnosis and/or activity activity and may be useful in the diagnosis.
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19-JUL-2000;
01-SEP-2000;
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Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humnomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                 Nucleic acids encoding polypeptides with useful in diagnosis and gene therapy -
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27-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                     Claim 20; Page 4310; 6221pp; English.
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                                                                                                                                                                                                                                                                                       Xue
                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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20-OCT-2000;
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, Wang D,
Yang Y,
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2000US-0560875.
2000US-0598075.
2000US-0520325.
2000US-0620325.
2000US-0634936.
2000US-0633561.
2000US-0593325.
2000US-0728422.
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D, Wang J, Zh
Wejhrman T,
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              leukaemia,
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, Zhang J, Ren
n T, Goodrich R;
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             nervous system disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder; carotid endarterectomy; vascular graft surgery; brain disorder; migraine; vascular injury; schizophrenia; eating disorder; depression; angioplasty; peripheral vascular disease; platelet aggregation; restenotic; embolism; thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein; G1; disseminated intravascular coagulation; thrombosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed Cas P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is corresponding cDNA molecule. P2Y12 receptor is corresponding cDNA molecule. P2Y12 receptor is expressed CC selectively in the platelets and brain, and couples to a pertussis toxin-CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for CC infarction, unstable angina, chronic stable angina, transient ischaemic CC infarction, unstable angina, chronic stable angina, transient ischaemic CC attacks, strokes, peripheral vascular disease, precelampsia, deep venous CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic CC thromboytopaenic purpura or a bleeding disorder; thrombotic and CC restentic complications following anaioplasty, carotid endarterectomy, CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery, carotid endarterectomy cost cabg (coronary artery bypass graft) surgery, vascular graft surgery, CC stent placements or insertion of endovascular devices and prostheses. CP2Y12 receptor is useful for identifying binding partners and for CC diagnostic applications. P2Y12 receptor provides targets for screening CC synthetic small molecules and combinatorial or naturally occurring CC synthetic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, vascular injury, or CC disease as well as schizophrenia, eating disorders, depression, migraine CC and other brain disorders. The present sequence is human P2-purinergic creating compound is a combinatoral platelet aggregation.
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Pred. No. 5e-187;
Pred. No. 5e-187;
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                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Method for screening anti-platelet agents with human ADP receptor PZTAC protein, its functional equivalent, or its homologous protein, as tool, for treating e.q. thrombotic or ischaemic diseases
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11-JAN-2001;
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                                                                               LCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                                                                           DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS
                                                                                                                                                                   IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI
                                       IIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-519236/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP receptor;
nic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL59205
                                                                                                                                                                                                                                                                                                                                                                       Page 48-49;
                                                                                                                                                                                                                                                                                                342 AA;
                                                                                                                                                                                                                                                       Conservative
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2001JP-0003577.
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RESULT 8
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                                                                                                                       The invention relates to identifying an ADP-glucose (ADP-G) receptor (a CC protein-coupled receptor) agonist, antagonist or ligand, comprises CC contacting the receptor with one or more candidate compounds so that the CC receptor produces a G protein-coupled signal in response to ADP-G or CC selectively binds ADP-G, and identifying the candidate molecule that CC alters signal production as an agonist, antagonist or binds as a ligand. CC Also included are altering signalling through an ADP-G receptor. By CC contacting a cell expressing the receptor with ADP-G or the ant/agonist, CC ameliorating an ADP-G receptor associated condition, by administering a CC individual and a composition comprising ADP-G or the ant/agonist to an CC individual and a composition comprising the ADP-G receptor and ADP-G composition induces vasorelaxation. The new methods are CC therapeutic composition induces vasorelaxation. The new methods are CC useful in identifying ant/agonists and ligands of the receptor. CC The ant/agonists are useful therapeutically for preventing or ameliorating conditions associated with the receptor such as CC cardiovascular disorders (e.g. ischaemia, hypertension, hypotension, CC angina pectoris, myocardial infarction, orthography congestive heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ADP-glucose; receptor; G protein-coupled receptor; agonist; antagonist; cardiovascular function disorder; vasorelaxation; asgonist; antagonist; cardiovascular function disorder; diarrhoea; ischaemia, angina pectoris; gastrointestinal disorder; disorder; immune disorder; immunodeficiency disorder; autoimmune disorder; rheumatoid arthritis; bacterial infection; viral infection; fungal infection; protozoal infection; respiratory disorder; asthma; kidney disorder; glomerulonephritis; hepatobiliary disorder; cirrhosis; endocrine disorder; adrenal dysfunction; musculoskeletal disorder; endocrine disorder; adrenal dysfunction; musculoskeletal disorder;
                                                           failure, shock, erectile dysfunction, orthostatic intolerance and migraine), gastrointestinal disorders (e.g. diarrhoea, gastritis, inflammatory bowel disease), immune disorders (e.g. immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis; nervous system disorder; Alzheimer's disease; psychotic disorder; depression; cancer; pain; glycogen storage disease; disorder of body weight, AIDS; acquired immunodeficiency syndrome; chromosome 3; Usher's syndrome type 3.
                disorders, autoimmune disorders, rheumatoid arthritis), infections caused by bacteria, fungi, protozoa or virus, respiratory disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying an agonist, antagonist or ligand of an ADP-glucose receptor, for treating cardiovascular, gastrointestinal, kidney, endocrine, immune disorders, and bacterial, viral, protozoal or fungal
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09-FEB-2001; 2001US-0780576.
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i, protozoa or virus, respiratory
bronchitis), kidney disorders (e.
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RESULT 9
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Best Local Similarity
Matches 342; Conserv
                                                                                                                                                                                                             Human; G protein coupled receptor; IGPcR17; analgesic; neuroleptic; tranquiliser; antiparkinsonian; neuroprotective; nootropic; anticonvulsant; metabolic; ancetic; anabolic; antiinflammatory; antidiarrheic; osteopathic; antiasthmatic; antiallergic; antiarthritic; immunosuppressive; gene therapy; psychiatric disorder; central nervous system disorder; movement dysfunction; schizophrenia; multiple sclerosis; Alzheimer's disease; kidney disease; obesity; gastrointestinal disorder; osteoporosis; infection;
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                                                                                                                                     Homo
                                                                                WO200202599-A2
                                                                                                                                                                                      gynecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human G protein-coupled receptor, IGPcR17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human or mouse G protein-coupled receptor protein, IGPcR17, useful diagnosis, prevention, amelioration or treatment of central nervous tem disorders such as Tourette's syndrome, Parkinson's disease and
                                                                                             IIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFF 300
                                                                                                                                                                       EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYPRTRGVGKVPKKKVNVKVFI 240
                                                                                                                                                                                                                                                    DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILINRQPRDKNVKKCSFLKS 180
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LCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM
                                     LCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETPM
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)B; ABA98535.
                                                                         IIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFF
                                                                                                                                                       EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFI
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1778; DB 2
Pred. No. 5e-187;
Mismatches (
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                                                                                                                                                                                                                                                             The present invention describes a method for identifying agonists and CC antagonists of mammalian G-Protein Coupled Receptor (GPCR) SP168 which CC may be used to treat neurodegenerative disorders. The method comprises: CC (a) contacting a mammalian SP168 receptor (or a functional fragment) in CC the presence of a known amount of a labeled SP168 receptor ligand with CC a sample to be tested for the presence of the SP168 receptor agonist or CC antagonist; and (b) measuring the amount of labeled SP168 ligand CC specifically bound to the receptor (the SP168 receptor agonist or CC antagonist in the sample is identified by measuring the difference in CC binding of the labeled SP168 receptor ligand to the receptor, compared CC to what would be measured in the absence of such agonist or antagonist). The method is used to detect agonists and antagonists (especially CC antibodies) of the SP168 GPCR which may be used to treat a neurodegenerative disorder, such as Parkinson's Disease, Allas) and CC multiple sclerosis (MS) in mammals, especially humans. The present
                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying modulators of mammalian G-Protein Coupled Receptor SP168, useful for treating Parkinson's Disease, Alzheimer's Disease, Huntington's Disease, amylotrophic lateral sclerosis and multiple sclerosis -
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                                                                                                                                                                                                           Sequence
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DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS
                                           IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI 120
                                                                                     MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60
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                           IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI
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1 MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI

Query Match Best Local Matches 34

Similarity

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Score 1778; DB 23; Pred. No. 5e-187; Mismatches 0;

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                   This invention describes a novel human platelet-activating factor (PAF) receptor-3 (PAFF-3) gene (I). The protein encoded by (I) probably modulates the activity of PAF, which is involved in many (patho)physiological processes e.g., thrombocyte activation, hypotension, increased vascular permeability, bronchoconstriction etc. (I), and derived (anti)sense oligonucleotides, are useful in the treatment and diagnosis of (I)-related diseases; for producing transgenic/knockout animals, and for recombinant expression of the protein (II) that it encodes. (II) is useful in ligand-binding studies and screening assays, also for treatment and diagnosis of (II)-related diseases. This sequence represents the human platelet-activating factor receptor (PAFR-3) protein described in the invention.
Sequence
                                                                                                                                                                                                                                            New human platelet-activating factor (PAF) receptor-3 diagnosis and treatment of PAF-related diseases
                                                                                                                                                                                                                                                                                      WPI; 2002-027296/04.
N-PSDB; AAI68802, AAI68803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bronchoconstriction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAFR-3; platelet activating factor receptor; human; chromosome thrombocyte activation; hypotension; vascular permeability;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PAFR3
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The 15625 receptor protein is a novel G-coupled protein receptor (GPCR). The cDNA for this protein was isolated by screening a human cDNA library with sequences homologous to other GPCRs. The 15625 receptor protein is expressed in the glial cells of the brain. It is also expressed in several other tissues. The 15625 receptor protein may be useful for producing antibodies which can be used to detect the presence of the receptor protein. The 15625 receptor protein polynucleotides are useful for generating probes, primers and antisense constructs. The polynucleotides encoding the 15625 receptor proteins can also be inserted into vectors to be used in gene therapy. The disorder that may be
                                                                                                                                                                                      coupled
                                                                                                                                                                                                                                          WPI; 2000-376543/32.
                                                                                                                                                                                                                                                                   Glucksmann MA,
                                                                                                                                                                                                                                                                                                                      06-NOV-1998;
25-AUG-1999;
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                                                                                                                                                Disclosure;
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                                                                                                                                                                      fying an agent modulating the level or activity of G-protein d receptor useful for screening a cell derived from a subject disorders such as anaemia, neutropenia and thrombocytopenia
                                                                                                                                                                                                                                                                                            MILLENNIUM
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                                                                                                                                                                                                                                                                                                                    98US-0187134.
99US-0382918.
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                                                                                                                                                                                                                                                                  Gu W,
                                                                                                                                             90-92; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of human 15625 receptor protein
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          N-PSDB;
                      WPI; 2001-418082/44.
                                             Hollopeter
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                                                        Ramakrishnan-Dubridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed CC as P2Y12 receptor and its corresponding CDNA molecule. P2Y12 receptor is case 12Y12 receptor and its corresponding CDNA molecule. P2Y12 receptor is case 12Y12 receptor is expressed CC selectively in the platelets and brain, and couples to a pertussis toxin CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor CC that responds to ADP. The invention also relates to a method for CC infarction, unstable angina, chronic stable angina, transient ischaemic CC infarction, unstable angina, chronic stable angina, transient ischaemic CC attacks, strokes, peripheral vascular disease, precelampsia, deep venous CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic CC restenotic complications following angioplasty, carotid endarterectomy, CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery, CC stent placements or insertion of endovascular devices and prostheses. CC P2Y12 receptor is useful for identifying binding partners and for CC disease as well as schizophrenia, eating disorders, depression, migraine CC compound libraries to regulate platelet aggregation, vascular injury, or Cd disease as well as schizophrenia, eating disorders, depression, migraine CC and other brain disorders. The present sequence is a fragment of human CC P2-purinergic receptor subtype, referred as P2Y12.
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 315; Conserv
          Murine; G protein-coupled receptor; IGPCR17; analgesic; neuroleptic; tranquiliser; antiparkinsonian; neuroprotective; nootropic; antiparkensonian; neuroprotective; nootropic; anticonvulsant; metabolic; ancettic; anabolic; antiinflammatory; antidiarrheic; osteopathic; antiasthmatic; antiallergic; antiarthritic;
                                                                                                      Murine G
                                                                                                                                          25-APR-2002
                                                                                                                                                                                                           AAM48354 standard;
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                                                                                                    protein-coupled receptor, IGPcR17.
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Pred. No. 3.2e-171;
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WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF TTRPFKTSSPSNLLGAKILSVVIWAFMFLISLPNMILTNRRPKDKDVTKCSFLKSEFGLV TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185 TVISDLLMILTFPFKILSDAKLGAGPLRTLVCQVTSVTFYFTMYISISFLGLITIDRYLK 131 TVISDLLMILTFPEKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 125 NTTFSPGTSTLCVRDYKITQVLFPLLYTVLFFAGLITNSLAMRIFFQIRSKSNFIIFLKN 71 NLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKN

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The present sequence is the protein sequence for murine G protein-coupled CC receptor (GPCR) protein, IGPCR17. The coding sequence for IGPCR17 is CC useful in gene therapy for prevention, amelioration or treatment of CC diseases characterised by aberrant expression or activity of IGPCR17, CC where the disease is a psychiatric or central nervous system (CNS) CC disorder associated with signal processing in CNS such as learning and CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias, CC dystonia, pain and spasms. In addition, IGPCR17 and its coding sequence CC are useful in diagnosis, prevention, amelioration or treatment of CC diseases associated with signal processing in CNS, schizophrenia, CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive CC diseases associated with signal processing in CNS, schizophrenia, CC disease, kidney diseases such as renal failure, obesity, CC disease, motility diseases such as irritable bowel syndrome (IBS), cC diarrhoea, motility disorders and conditions of delayed gastric emptying, osteoporosis, infections such as bacterial, fungal, protozoal and viral confections, asthma, allergy, arthritis, sepsis and gynecological
   Matches
                      Query Match
Best Local
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                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human or mouse G protein-coupled receptor protein, IGPcR17, useful for diagnosis, prevention, amelioration or treatment of central nervous system disorders such as Tourette's syndrome, Parkinson's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-140080/18.
N-PSDB; ABA98539.
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                        Similarity
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   Conservative
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                    87.5%;
88.7%;
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   16;
 Score 1555.5; DB 23
Pred. No. 1.6e-162;
.6; Mismatches 21;
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                                       DB 23;
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                               The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed CC selectively in the platelets and brain, and couples to a pertussis toxin-CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor CC that responds to ADP. The invention also relates to a method for CC infarction, unstable angina, chronic stable angina, transient ischaemic CC infarction, unstable angina, chronic stable angina, transient ischaemic CC attacks, strokes, peripheral vascular disease, precelampsia, deep venous CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic CC restenotic complications following angioplasty, carotid endarterectomy, CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery, CC stent placements or insertion of endovascular devices and prostheses. CC P2Y12 receptor is useful for identifying binding partners and for CC adagnostic applications, P2Y12 receptor provides targets for screening CC compound libraries to regulate platelet aggregation, vascular injury, or Cd disease as well as schizophrenia, earting disorders, depression, migraine CC and other brain disorders. The present sequence is rat P2-purinergic CC receptor subtype, referred as P2Y12 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 81-82; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications
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N-PSDB; AAD08693.
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Hollopeter G;
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                                                      FICEVPFHFARIPYTLSQTRAVEDCNAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF
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   DB
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US-09-521-456-2
US-09-528-740-2
US-08-812-871-1
US-08-467-947A-29
US-08-98-876-3
US-08-98-876-3
US-08-98-876-3
US-08-98-876-3
US-08-98-876-3
US-08-98-876-947A-6
US-08-98-876-9
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US-08-98-3750-4
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	SLNACLDPFIYFF 300		YISISFLGLITI 120	IRSKSNFI	gth 342; els 0; Gaps			Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl Sequence 2, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 61, Appli Sequence 61, Appli Sequence 61, Appli Sequence 61, Appli
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RESULT 2 US-09-221-456-2 ; Sequence 2, Application US/09221456

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GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
ALISON
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TELEX: 846169
INFORMATION FOR SEQ ID NO:
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FILING DATE: 23-OCT-1997
ATTORNEY_AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23.031
REFERENCE/DOCKET NUMBER: GH-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATING:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEAA81 RECOMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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CITY: Valley Forge
STATE: PA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
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                                                               VPYTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLIYIFLCKKFTEKLPCMQ--G
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O. Box 980
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US-09-558-740-2
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LENGTH: 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.3%; Score 823; DB 4; Best Local Similarity 48.7%; Pred. No. 5.9e-63; Matches 154; Conservative 57; Mismatches 103
                                                                                      GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND TITLE OF INVENTION: ANTAGONISTS OF THE HNEAAB1 RECEPTOR FILE REFERENCE: GH-70318-2 CURRENT APPLICATION NUMBER: US/09/558,740 CURRENT FILING DATE: 2000-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHAMBERS, JON APPLICANT: SZEKERES, PHILIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SATHE, APPLICANT: HALSE APPLICANT: MUIR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 333
TYPE: PRT
                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                        313
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STREET: 317
CITY: Palo
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                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                      RKTTASSQENHSSQTD 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPVFAKTVSIFIWFFLFFISLPNTILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HALSEY, WENDY MUIR, ALISON
                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Dr.
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

Diskette

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USA

STATE: CA

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RESULT 5
US-08-467-948A-29
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                                                                                                Sequence 29, Application US/08467948A Patent No. 5998164
GENERAL INFORMATION:
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Best Local Similarity 47.8%;
Matches 151; Conservative 5
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 333 amino acids
TYPE: amino acid
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     APPLICANT:
                                                                 APPLICANT:
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LIBRARY: MMLR3
CLONE: 568987
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FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                   APPLICANT:
                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                             135
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REGISTRATION NUMBER: 36,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CPRDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYLKNTLVADLIMTLM 74
                                                                                                                                                                                                                                             NSATSLSQDNRKKEQD 332
                                                                                                                                                                                                                                                                             VPYTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLISIFLCKKFTEKLPCMQ--G
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                                               LI, YI
CAO, LIANG
NI, JIAN
GENTZ, REINER
BULT, CAROL J.
SUTTON III, GRANGER G.
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Pred. No. 9.8e-61;
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; STRANDEDNESS: single ; TOPOLOGY: not relevant ; MOLECULE TYPE: peptide US-08-467-948A-29
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTER/STICS:
LENGTH: 325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: FLOPPY
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TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
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302
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COUNTRY:
                                                                                                                                246 FICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF 305
                                                                                                                                                                               182 WHKASNYIFVAIFWIVFLLLIVFYTAITKKIFKSHLKŚSRNSTSVKKKSSRNIFSIVFVF 241
                                                                                                                                                                                                                                                                   122 IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 181
                                                                                                                                                                                                                                                                                                                                                         62 IVIADEVMSITEPEKILGDSGLGPWQLNVEVCRVSAVLEYVNMYVSIVEEGLISEDRXXK 121
                                                                                                                                                                                                                                                                                                                                                                                 66 TVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVTSVIEVETMYISISELGLITIDRYQK 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 43.4%; Score 772; DB 2; Local Similarity 47.5%; Pred. No. 1.3e-58; les 149; Conservative 60; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                        TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185
  REILCKKLHIPLKA
                                            RNSLISMLKCPNSA 319
                                                                                      FVCFVPYHIARIPYTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPF 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSTSTQPPDESCSQNLLITQQIIPVLYCMVFIAGILLNGVSGWIFFYVPSSKSFIIYLKN 61
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RESULT 6
US-08-467-947A-29
; Sequence 29, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:

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Best Local Similarity 47.5
Conservative
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INFORMATION FOR SEQ ID NO: 29:
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ADDRESSEE: STERNE, KESSLER,
STREET: 1100 NEW YORK AVE.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BULT, CAROL J.

APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: Polynucleotides Encod

TITLE OF INVENTION: Coupled Receptor GPR1

NUMBER OF SEQUENCES: 30
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ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-371-2600
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MEDIUM TYPE: FLOPPY
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 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPAYIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-JU
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                              RNSLISMLKCPNSA 319
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REILCKKLHIPLKA 315
                                                               FVCFVPYHIARIPYTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPF
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BULT, CAROL J.
SUTTON III, GRANGER G.
ROSEN, CRAIG A.
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US-08-988-876-8
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APPLICANT:
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MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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APPLICATION NUMBER:
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                 246 FICEVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF
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OPERATING SYSTEM:
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CITY: Palo Alto
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CLONE: 285995
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                                                                                                                 IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 182
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Hillman, Jennifer L.
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TYPE: PRT
ORGANISM: Homo sapiens
US-09-303-524A-2
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                                                               Sequence 3, Application Patent No. 6063596
GENERAL INFORMATION:
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LENGTH: 338
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                                                                                                Application US/08988876
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VENTION: METHODS OF SCREENING FOR AGONISTS AND
VENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
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SARAU, HENRY M.
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                    Lal, Preeti
Bandman, Olga
Hillman, Jennifer L.
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RESULT 10
US-08-467-948A-6
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ZIP: 94304
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Query Match 38.2%; Score 679.5; DB 3; Best Local Similarity 43.7%; Pred. No. 1.1e-50; Matches 132; Conservative 64; Mismatches 99;
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                         244 VFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                             25 NRSDGPGKNTTL---HNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 NLTSAPG-NTSLCTRDYKITQVLFPLLYTVLFFYGLITNGLAMRIFFQIRSKSNFIIFLK 64
                                                                                                                                      VWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRK-KVNVKVFIIIA 243
VYFTCFLPYHLCRMPSTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPIIYFFMCR 319
                                                                                                    KWHTAVTYVNSCLFVAVLVILIGCYIAISRYIHKS--SRQFISQSSRKRKHNQSIRVVVA 259
                                                                                                                                                                                                                                                                                                                                                                     NTVISDLLMILTEPEKILSDAKLGTGPLRTEVCQVTSVIFYFTMYISISFLGLITIDRYQ 124
                                                                                                                                                                                                            KVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGV 201
                                                                                                                                                                                                                                                              KTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGL 184
                                                                                                                                                                                                                                                                                                                   NIVVADLIMTLTFPFRIVHDAGFGPWYFKFILCRYTSVLFYANMYTSIVFLGLISIDRYL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 amino acids
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linear
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US-08-467-947A-6
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GENERAL INFORMATION:
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APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS: STEPPINE KESSIFF GOIDERTEIN & FOX B I I C.
ANDERSSEP. STEPPINE KESSIFF GOIDERTEIN & FOX B I I C.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
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APPLICANT:
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APPLICATION NUMBER: PCT/US95/04079
FILLING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140
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MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                                                                   137 NLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV 196
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                                                                                                                                                                                                                                                                                                                                                     77 FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                                                                                                                                                                                                                                               15 CPKDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYLKNTLVADLIMTLM 74
                                                                                                                                                                                                                                                                                                                                                                                                                                       17 CTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLIMILT 76
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                                                                                                                                                         IFWTVFILMLVFYVVIAKKYMILIESPKVRTEKTKSWKAKYLLSWLSSLCVLLHFISPE
                                                                             FHILTVKPTIRLT---VDCKI-NCLLLKKQLSFW 284
                                                                                                                      FHFARIPYTLSQTRDVFDCTAENTLFYVKESTLW 285
                                                                                                                                                                                                      IFWINFLIVIVCYTLITKE----LYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVP- 251
                                                                                                                                                                                                                                             KPVWGKTVSIFIWFFWFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNICQF 194
                                                                                                                                                                                                                                                                                                                               LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
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NI, JIAN
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Matches 116;
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NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
THE TOTAL OF THE TOTAL O
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APPLICATION NUMBER: PCT/I
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES: 30
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APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER
APPLICANT: ROSEN, CRAIG A.
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                                                                                                                                                      195
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255
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CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 CTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLLMILT 76
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                                                                                                                                                                                                                                                                                                                                               NLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
FHILTVKPTIRLT---VDCKI-NCLLLKKQLSFW 284
                                                                       FHFARIPYTLSQTRDVFDCTAENTLFYVKESTLW 285
                                                                                                                                                                                                                         IFWINFLIVIVCYTLITKE----LYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVP- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPKDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIIYLKNTLVADLIMTLM 74
                                                                                                                                              IFWTVFILMLVFYVVIAKKYMILIESPKVRTEKTTKSWKAKYLLSWLSSLCVLLHFISPE
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16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT/US95/04079
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RESULT 12

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Best Local Similarity
Matches 112; Conserv
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikk1
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                           180
                                                                                                                                                                            190
                                                                                                                                                                                                           120 CKIYRIQEPGFAKMISTVVWLMVLLIMVPNMMIPIKDIKEKSNVGCMEFKKEFGRNWHLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMBINATE: Macridge
                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                    13 NTSLCTRDYKITQYLFPLLYTYLFFYGLITNGLAMRIFFQIRSKSNFI-IFLKNTVISDL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/702,344 FILING DATE:
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                                                                                                                                     THEICVAIF-LNESAILLISHCLVIRQLYRN----KDNENYPNVKKALINILLVTTGYII
                                                                                                                                                                      VNYICQVIEWINE-LIVIVCYTLITKELYRSYVRTRGVGKVPR-KKVNVKVFIIIAVEFI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28, 5723315
                                                                                                   CFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFTYFFLCKSFRN 307
                                                                                                                                                                                                                                                                               LITLALPYKIVVD--LGVAPWKLKIFHCQVTACLIYINMYLSIIFLAFVSIDRCLQLTHS 119
                                                                                                                                                                                                                                                                                                                                                     NSSFFCPVKDLEP-FTYFFYLVFLVGIIGSCFATWAFIQKNTNHRCVSIYLINLLTADF
KVTETFASPKETKAQKEKLRCENNA 319
                                  SLI----SMLKCPNSA 319
                                                                     CFVPYHIVRIPYTLSQTEVITDCSTRISLFKAKEATLLLAVSNLCFDPILYYHLSKAFRS
                                                                                                                                                                                                                                            FKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEI 189
                                                                                                                                                                                                                                                                                                                LMILTFPFKILSDAKLGTGP--LRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319 amino acids
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87 CambridgePark Drive
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--11te, Edward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                       27.4%; Score 488; DB 1; I
34.5%; Pred. No. 2.2e-34;
vative 62; Mismatches 125;
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US-08-118-270-39
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Patent No. 5508384
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MUF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 208-737-3528
TELEX: 248622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                     314
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                           27 LEPLLYTVLFEVGLITNGLAMRIFEQI-RSKSNEI-IFLKNTVISDLLMILTEPEKILSD 84
                                                                                                                                                                                                                                                                                                                                                          Match 23.1%; Score 410.5; DB 1; Local Similarity 32.2%; Pred. No. 9.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 326 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                 QVI-FWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFH
                                                                                                                                                                                                             SLVIWVAIVAAASYFLVMMDSTNVVSNKAGSGNITRC-FERYEKGSKPVLIIH----IC
NIMRSSQKCSRVTRDTGTEMAIPINHTPV
                                   KCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                    MVQLPWTLAEL-GMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFRKHLSEKL
                                                                                                      FARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISML
                                                                                                                                           IVLGFFIVFLLILFCNLVIIHTLLRGPVKQQRNAEV-RRRALWMVCTVIAVFVICFVPHH
                                                                                                                                                                                                                                                   SVVIW-----AFMFLLSLPNMILINROPRDKNVKKCSFLKSEFG----LVWHEIVNYIC 194
                                                                                                                                                                                                                                                                                      SNQGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPIKTAQATTRKRGIAL 120
                                                                                                                                                                                                                                                                                                                         AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murphy, Randall B.
Schuster, David I.
SCHUSTER, DAVID I.
VENTION: POLYPEPTIDES OF
VENTION: RECEPTORS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF G-COUPLED PROTEIN
ND COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Best Local
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GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCE:

CORRESPONDENCE ADDRESS:

PROWDY AND NEIMARK

PROWDS AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US93/08528 FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                     175
                                                                                                                                                                                                                               121
                                                                                           254 FARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISML 313
                                                                                                                                                                                                                                                              145
293 NIMRSSQKCSRVTRDTGTEMAIPINHTPV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                                              27 LFPLLYTVLFFVGLITNGLAMRIFFQI-RSKSNFI-IFLKNTVISDLLMILTFPFKILSD 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 248633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         1 LFPIVYSIIFVLGIIANGYVLWVFARLYPSKKNEIKIFMVNLTVADLLFLITLPLWIVYY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocal Similarity
                                  KCPNSATSLSQDNRKKEQDGGDPNEETPM 342
                                                                     MVQLPWTLAEL-GMWPSSNHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFRKHLSEKL
                                                                                                                                               IVLGFFIVFLLILFCNLVIIHTLLRGPVKQQRNAEV-RRRALWMVCTVIAVFVICFVPHH
                                                                                                                                                                                  QVI-FWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFH 253
                                                                                                                                                                                                                         SLVIWVAIVAAASYFLVMMDSTNVVSNKAGSGNITRC-FERYEKGSKPVLIIH-----IC 174
                                                                                                                                                                                                                                                            SVVIW-----AFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFG----LVWHEIVNYIC 194
                                                                                                                                                                                                                                                                                                 SNOGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITYNRFQAVKYPIKTAQATTRKRGIAL 120
                                                                                                                                                                                                                                                                                                                                  AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.18; 32.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version
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Pred. No. 9.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 300
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US-08-988-876-9
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APPLICANT: Lal, pr
APPLICANT: Bandman
APPLICANT: Hillman
APPLICANT: Yue, He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Applic Patent No. 6063596
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED TITLE OF INVENTION: WITH IMMUNE RESPONSE NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
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OPERATING SYSTEM:
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CLONE: 49443
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CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                   Match 22.1%; Score 392.5; DB 3; Local Similarity 30.7%; Pred. No. 3.4e-26;
ICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFR 306
                                                ----ICIVLGFFIVFLLILFCNLVIIHTLLRQPVKQQRNAEV-RRRALWMVCTVLAVFV 242
                                                                                                                 TRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNKAGSGNITRC-FEHYEKGSKPVLIIH 188
                                                                                                                                                                               FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
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                                                                               EIVNYICQVI-FWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFF 246
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Hillman, Jennifer L.
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// cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep: *
// cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
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10 US-9-964-008-3
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12 US-9-769-159-2
13 US-9-826-508-20
14 US-9-826-508-20
15 US-9-919-172-22
16 US-9-919-172-22
17 US-10-025-335-1
2 US-10-025-335-1
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ALIGNMENTS

US-09-964-008-1

Sequence 1, Application US/09964008 Patent No. US20020156246A1

밁 δ 밁 Qy 밁 Q 片 US-09-964-008-1 ; SOFTWARE: PatentIn Ver. ; SEQ ID NO 1 ; LENGTH: 342 ; TYPE: PRT ; ORGANISM: Homo sapiens GENERAL INFORMATION: Query Match 100.0%; Score 1778; DB 9; Best Local Similarity 100.0%; Pred. No. 5.8e-151; Matches 342; Conservative 0; Mismatches 0; APPLICANT: Gu, Wei
TITLE OF INVENTION: 15625 Receptor, A No. US20020156246Alel G-Protein Coupled Rece
FILE REFERENCE: 5800-13, 035800-171548
CURRENT APPLICATION NUMBER: US/09/964,008
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/187,134
PRIOR APPLICATION NUMBER: 09/187,134
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 5 APPLICANT: Glucksmann, Maria A. APPLICANT: Gu, Wei 181 181 121 121 DRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKS 180 ITAVFFICEVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFTYFF EFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFI 240 Ver. 2.0 Length 342; Indels 0; Gaps 240 0

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US-09-827-937A-2
; Sequence 2, Application US/09827937A
; Patent No. US20020052043A1
; GENERAL INFORMATION:
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US-09-835-922-2
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; Patent No. US20010046497A1
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Matches 342;
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LENGTH: 342
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APPLICANT: L1, Y1
APPLICANT: Ruben, Steven M.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human G-Protein Coupled
FILE REFERENCE: 1488.1220003
CURRENT APPLICATION NUMBER: US/09/827,937A
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 08/852,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/835,922
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: US 60/199,041
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhang, Fang L.
APPLICANT: Luo, Lin
APPLICANT: Gustafson, Eric
APPLICANT: Liu, Yan-Hui
APPLICANT: Chen, Guodong
TITLE OF INVENTION: G-Protein Coupled Receptor
FILE REFERENCE: CN01167K
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Pred. No. 5.8e-151;
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LENGTH: 342
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
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ORGANISM: Homo
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; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-780-576-2
                                                                                                                                                                                                                                                             APPLICANT: Civelli, Olivier
APPLICANT: No. US20020072072A1hacker, Hans-Peter
APPLICANT: Wang, Zhiwei
APPLICANT: Reinscheid, Rainer
TITLE OF INVENTION: ADP-Glucose Receptor
FILE REFERENCE: P-UC 4530
CURRENT APPLICATION NUMBER: US/09/780,576
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/234,025
PRIOR TILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US Patent No. US20020072072A1
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Best Local Similarity 100.0%;
Matches 342; Conservative 0
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                                                               MQAVDNLTSAPGNTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI
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                                                                                                                         Score 1778; DB 10;
Pred. No. 5.8e-151;
; Mismatches 0;
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Pred. No. 5
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5.8e-151;
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US-09-964-008-3
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APPLICANT: Glucksmann, Maria A.
APPLICANT: Gu, Wei
TITLE OF INVENTION: 15625 Receptor, A NO.
FILE REFERENCE: 5800-13, 035800-171548
CURRENT APPLICATION NUMBER: US/09/964,008
CURRENT FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 342
Sequence 2, Application US/09769159
Patent No. US20010021509A1
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH M.
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Best Local Similarity
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PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 5
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ORGANISM: Macaca
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98.0%;
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Pred. No. 2.7e-148;
3; Mismatches 4;
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                       Sequence 1, Application US/0984889

Patent No. US20020025555A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
APPLICANT: Cheng, Muzong
TITLE OF INVENTION: GPCR DIAGNOSTIC FOR BRAIN CAN
FILE REFERENCE: PC-0042 CIP
CURRENT APPLICATION NUMBER: US/09/848,889

CURRENT FILING DATE: 2001-05-03

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PERL Program

SEQ ID NO 1

LENGTH: 333
TYPE: PRT
ORGANISM: Homo sapiens
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; SOFTWARE: FRASTSEQ FOR WI
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-769-159-2
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US-09-848-889-1
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CURRENT APPLICATION NUMBER: US/09/769,159
CURRENT FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR APPLICATION NUMBER: 09/558,740
PRIOR APPLICATION NUMBER: 09/558,740
PRIOR FILING DATE: 2000-04-26
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Best Local
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NAME/KEY: misc_feature
OTHER INFORMATION: Inc
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US20020025555A1
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US-09-919-497-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 77
LENGTH: 338
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MUTTER, GEOIGE L.

APPLICANT: MUTTER, GEOIGE L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
   246 FICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF
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                                                                               WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF 245
                                                                                                                             IVKPLWTSFIQSVSYSKLLSVIVWMLMLLLAVPNIILTNQSVREVTQIKCIELKSELGRK 182
                                                                                                                                                      TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLV 185
                                                                                                                                                                                                     IVIADEVMSLTEPEKILGDSGLGPWQLNVEVCRVSAVLEYVNMYVSIVFFGLISFDRYYK 122
                                                                                                                                                                                                                                                                              NSTSTQPPDESCSQNLLITQQIIPVLYCMVFIAGILLNGVSGWIFFYVPSSKSFIIYLKN 62
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                                                          WHKASNYIFVAIFWIVFLLLIVFYTAITKKIFKSHLKSSRNSTSVKKKSSRNIFSIVFVF 242
                                                                                                                                                                                                                                                                                                                NLTSAPGNTSLCTRDYKITQVLEPLLYTVLEFVGLITNGLAMRIFFQIRSKSNFIIFLKN 65
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US-09-826-508-10
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NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 358
TYPE: PRT
                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nabil Elshourbagy
APPLICANT: Lisa Vawter
                                                                                                                                                                                                                                      Sequence 10, Application US/09826508 Patent No. US20010025099A1
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                                                                                     TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides TITLE OF INVENTION: and Polynucleotides FILE REFERENCE: GP-70744USB CURRENT APPLICATION NUMBER: US/09/826,508 CURRENT FILING DATE: 2001-04-05
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CURRENT APPLICATION NUMBER: US/09/826,508
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 338
TYPE: PAT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.7%; Score 741.5; DB 10; Best Local Similarity 44.1%; Pred. No. 7.6e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides TITLE OF INVENTION: and Polynucleotides FILE REFERENCE: GP-70744USB
                                                                                                                                             244 VFFICEVPEHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCK 303
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                                                    SFR---NSLISM-LKCPNSATSLSQDNRKKE 330
                                                                                                                                                                                                                                                                                                                                                                                                            QKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFG 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRY 123
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                                                                                                                 VFVVCFVPYHIARIPYTKSQTEGHYSCRTKETLLYAKEFTLLLSAANVCLDPIIYFFLCQ
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US-09-974-298-86
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PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 86
LENGTH: 358
TYPE: PRT
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Best Local :
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APPLICANT: Chen, Hu
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CURRENT APPLICATION UNDER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020156263A1 1650519CD1
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                  185
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Local Similarity 42.2%;
nes 139; Conservative (
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les 132; Conserv
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                                                                                                VFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCK 303
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                                                                                                                                                           NRSDGPGKNTTL---HNEFDTIVLPVLYLIIFVASILLNGLAVWIFFHIRNKTSFIFYLK 81
                                                                                                                                                                            NLTSAPG-NTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIIFLK 64
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                                           KVVKPFGDSRMYSITFTKVLSVCVWVIMAVLSLPNIILTNGQPTEDNIHDCSKLKSPLGV
                                                         KTTRPEKTSNPKNLLGAKILSVVIWAFMELLSLPNMILTNRQPRDKNVKKCSFLKSEEGL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFFTCFLPYHLCRIPFTFSHLDRLLDESAQKILYYCKEITLFLSACNVCLDPIIYFFMCR 319
                                                                                                                               NTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQ 124
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                                                                                                                                                                                                                                 38.2%; Score 679.5; DB 9
                                                                                                                                                                                                                     64; Mismatches
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Pred. No. 1.2e-54;
8; Mismatches 113
                                                                                                                                                                                                                                             DB 9;
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PRIOR APPLICATION UNMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGRAM
SEQ ID NO 22
LENGTH: 358
TYPE: PRT
                                                                                         Sequence 1, Application US/10025335
Patent No. US20020127648A1
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
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US-09-919-172-22
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US-10-025-335-1
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TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Faris, Mary
APPLICANT: Turner, Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20020119463A1 1650519CD1
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                         Bandman, TITLE OF INVENTION:
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SF 321
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132; Conserv
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SEQUENCES:
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NOVEL HUMAN C5A-LIKE RECEPTOR: 3
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Pred. No. 2.6e
54; Mismatches
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2.6e-53;
les 99;
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RESULT 14
US-10-084-206-3
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Sequence 3, Application US/10084206 Patent No. US20020106741A1 GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
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                                                                                                                                          295 KVTETFASPKETKAQKEKLRCENNA 319
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/025,335
FILING DATE: 18-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                    SLI------SMLKCPNSA 319
                                                                                                                                                                                                                                                                  CFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRN 307
                                                                                                                                                                                                                                                                                                                                                                                              CKIYRIQEPGFAKMISTVVWLMVLLIMVPNMMIPIKDIKEKSNVGCMEFKKEFGRNWHLL
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SOFTWARE: FastSEQ for Windows Version
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STATE: CA
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STRANDEDNESS: single
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0198
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Pred. No. 2.4e-36;
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                                                                                                                                                                               SOFTWARE: PatentIn Ver. SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09827937A Patent No. US20020052043A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 104;
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                                                        Query Match
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               Matches
                                    Best Local Similarity
                                                                                                                                                                                                                                        TITLE OF INVENTION: Human G-Protein Coupled EILE REFERENCE: 1488.1220003
CURRENT APPLICATION NUMBER: US/09/827,937A
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 08/852,824
PRIOR FILING DATE: 1997-05-07
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Li, Y1
APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/084,206
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US95/07288
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 08/468,534
PRIOR FILING DATE: 1995-06-06
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 18
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SOFTWARE: PatentIn Version 3.1
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TITLE OF INVENTION: G-Protein Receptor HTNAD29
FILE REFERENCE: PF191D1C1
                                                                                                              LENGTH: 348
TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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               94;
               Conservative
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                                  21.1%; Score 376; DB 10; 26.1%; Pred. No. 2.4e-26;
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Pred. No. 3.6e-27;
               Mismatches
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Run on:

Title: Perfect score: Sequence: US-09-835-922-2 1778 1 MQAVDNLTSAPGNTSLCTRD.....SQDNRKKEQDGGDPNEETPM 342

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

332 332 332 332 332 332 332 332 332 332	11 11 11 11 11 11 11 11 11 11 11 11 11	Result No.
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Takasaki J., Kamohara Ohishi T., Soga T., M. "Molecular cloning of pharmacological compa receptor."; MO1. Pharmacol. 60:43 [4] MO1. Pharmacol. 60:43 [4] SEQUENCE FROM N.A. Reinscheid R.K., Noth Civelli O.; "ADP-glucose activate: smooth muscle contract submitted (OCT-2000) SEQUENCE FROM N.A. Takeda S., Kadowaki S "Identification of G	TISSUE-HYPOTHALAMUS; MEDLINE-21269433; PU Zhang F.L. Luo L., Liu YH., Chen G., MONSMA F.J. Jr.; "ADP is the cognate SP1999."; J. Biol. Chem. 276:8 [3] [3] [3] [3] MEDLINE-21194281; PU MEDLINE-21194281; PU	NCBI_TaxID=9606; [1]TaxID=9606; SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=21037966; Pubmedilopeter G., Jantzen Ramakrishnan V., Yang I Conley P.B.; "Identification of the antithrombotic drugs." Nature 409:202-207(200:	UMAN 2YC_HUMAN 2YC_HUMAN 9H244; 5-JUN-200 5-JUN-200 2Y purinc 2Y purinc 2Y purinc 2X plue 2Plue 2Plue 2Plue 2Plue 3Plue
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Zeng J., Ehlert F.J., receptor and inhibits DBJ databases. Mitaku S.; cor genes from the human	J., Smith M., Qiao X., Palmer K., Bayne M., protein-coupled receptor	; HOMINICAE; HOMO. , Li G., England L., Nurden A., Julius D.J., ptor targeted by) ADP recep 2Y(cyc))

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R PRINTS; PROUD237; GC_PROTEIN_RECEP_F1_1; FALSE_NEG.

R PROSITE; PSO0237; GC_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PSO0237; GC_PROTEIN_RECEP_F1_2; 1.

R PROSITE; PSO0237; GC_PROTEIN_RECEP_F1_1; FALSE_NEG.

PROSITE; PSO0237; GC_PROTEIN_RECEP_F1_1; FALSE_NEG.

R PROSITE; PSO0237; GC_PROTEIN_RECEP_F1_1; FALSE_NEG.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-Prostate;
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TISSUE SPECIFICITY: Highly expressed in the platelets, lower levels in the brain. Lowest levels in the lung, appendix, pituitary and adrenal gland. Expressed in the spinal cord and the fetal brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
IFLKNTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF313449;
AF321815;
AB052684;
AF310685;
AB083596;
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Q9NC3; Q9BGT8;

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P2Y purinoceptor 12 (P2Y12).

P2RY12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Frontal cortex, and Medulla oblongata; Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae; Macaca. NCBI_TaxID=9541;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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- SUBCELLULAR
- SIMILARITY:
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                                      RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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Kakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kakota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kakota K., Matsuda H.A., Ashburner M., Wagner L., Washio T.,

Kakota K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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Sakai K., Sakai K., Okido M., Foolina M., Sakai M., Sakai K., Sa
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Mammalia; Eutheria; F
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P2RY12.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-C57BL/6J; 1
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
P2Y purinoceptor 12 (P2Y12).
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EMBL; AK014807; BAB29501.1; -.
EMBL; BC025428; AAH25428.1; -.
EMBL; BC027381; AAH27381.1; -.
MCD; MGI:1918089; P2TY12.
InterPro; LPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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PRINTS; PR01559; PZX12PRNCPTR.
PRINTS; PR01555; UDPGLUCOSER.
PROSITE; PS00237; G_PROTEIN_RECE
PROSITE; PS50262; G_PROTEIN_RECE
G-protein coupled receptor; Transcription
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CONFLICT
SEQUENCE
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les 299; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane; Glycop;
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Pred. No. 1.2
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"Identification of the platelet ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE KNUM .... STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
MEDLINE-21037966; PubMed-11196645;
MEDLINE-2103796; PubMed-1103796; PubMed-11196645;
MEDLINE-2103796; PubMed-11196666; PubMed-11196666; PubMed-11196666; PubMed-11196666; PubMed-11196666; PubMed-11196666; PubMed-11196666; PubMed-11196666; PubMed-11196666
                                                                                                               DOMAIN
TRANSMEM
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Nature 409:202-207(2001).
-i- FUNCTION: Receptor for ADP and ATP cinhibit the adenylyl cyclase second
                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                 PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR011564; OGRIRECEPTOR.
PRINTS; PR011569; P2Y12PRNCPTR.
PRINTS; PR01655; UDPGLUCOSER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet A
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                                                                                                                                                                                                                                                           receptor;
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TO FAMILY 1 OF G-PROTEIN COUPLED
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15-JUL-1998
15-JUN-2002
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SEQUENCE
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Mammalia; Eutheria;
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Q15391;
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343 AA;
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NOMIZE N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.; "Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0001-KIAA0040) deanalysis of randomly sampled cDNA clones from human immating cell line KG-1.";
Chambers J.K., Macdonald L.E., Sarau H.M., Ames R.S., Free Foley J.J., Zhu Y., McLaughlin M.M., Murdock P., McMillan Trill J., Swift A., Alyar N., Taylor P., Vawter L., Naheed Szekeres P., Hervleu G., Scott C., Watson J.M., Murphy A.J Klein C., Bergsma D.J., Wilson S., Livi G.P.;
                                                                                                                                                            MEDLINE-21426338; PubMed-11524702;
Joensuu T., Haemaelaeinen R., Yuan B., Johnson Gasparini P., Zelante L., Pirvola U., Pakarine de la Chapelle A., Sankila E.-M.;
"Mutations in a novel gene with transmembrane syndrome type 3.";
Am. J. Hum. Genet. 69:673-684(2001).
                                                                                                     MEDLINE=20219108; PubMed=10753868;
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(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
receptor (G protein-coupled recep
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86.9%;
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Pred. No. 7.5
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7AE0AFCE66674136 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catarrhini;
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Pakarinen
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Matches
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Best Local
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PROSITE; PS0023
PROSITE; PS5026
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J. Biol. Chem. 275:10767-10771(2000).

-i- FUNCTION: Receptor for UDP-glucose and other UDP-sugar coupled G-proteins. Not activated by ATP, ADP, UTP or ATP.

-i- SUBCELLULAR LOCATION: Integral membrane protein.

-i- TISSUE SPECIFICITY: Highest expression in the placenta, adipose tissue, stomach and intestine, intermediate levels in the brain spleen, lung and heart, lowest levels in the kidney.

-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CARBOHYD
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TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                    WHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVF
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REILCKKLHIPLKA 316
                                 RNSLISMLKCPNSA 319
                                                              FVCFVPYHIARIPYTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPF
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PS50262;
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CYTOPLASMIC (POTENTIAL)
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BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL)
N-LINKED (GLCNAC. ..) (POTENTIAL);
8DBE7C782CB4753D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 772;
Pred. No. 3
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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Q
                                                                 RESULT 6
P2YX_MOUSE
                           Query Match
Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        progenitors.";
Submitted (AUG-1999) to
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                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UDP-glucose
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
receptor (G protein-coupled receptor
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor for UDP-glucose
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                                    41.78;
44.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ databases
                                                                 MW;
                            69;
                                                               7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . ) (POTENTIAL);
4376B50622A68A4E CRC64;
                                    Score 741.5;
Pred. No. 3.
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss institute of Bioinformatics and the EMBL outset the European Bioinformatics institute. There are no restrictions the property of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charlton M.E., Williams A.S., Fogliano M., Sweetnam P.M., Du Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Receptor for UDP-glucose coupled to G-proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
7 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. . .) (
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Probable G protein-
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Peripheral blood monocytes;

MEDLINE-98036061; PubMed-9370294;

Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.

Golden-Fleet M., Kelleher K., Kriz R., LaVallie E.R.,

Spaulding V., Stover J., Williamson M.J., McCoy J.M.;

"A genetic selection for isolating cDNAs encoding seco
EMBL; AF002986; AAC51846.1; -. EMBL; AF411849; AAL47763.1; -. InterPro; IPR000276; GPCR_Rhod
                                                                                                                                                                                                                                                                                                                                                                                                                                  Joensuu T., Haemaelaeinen R., Yuan B.,
Gasparini P., Zelante L., Pirvola U., I
Gasparini P., Sankila E.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              "Mutations in a novel gene with transmembrane syndrome type 3.";
Am. J. Hum. Genet. 69:673-684(2001).
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MEDLINE=21426338; PubMed=11524702;
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Pred. No. 5e-40;
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
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PRINTS; P
PROSITE;
PROSITE;
Schoneberg T., Schulz A., Grosse R., Schade R., Schultz G., Gudermann T.;
Ra novel subgroup of class I G-protein-coupled Biochim. Biophys. Acta 1446:57-70(1999).

-I- FUNCTION: ORPHAN RECEPTOR.
                                                                     Eukaryota; Metazoa; Chordata; Mammalla; Eutheria; Rodentia; NCBI_TaxID=10090;
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SEQUENCE
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DOMAIN
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MEDLINE-99326137; PubMed-10395919;
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                                                                                                          musculus
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S; PR00237;
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PS50262;
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02 (Rel. 41, Last
3 protein-coupled
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7; GPCRRHODOPSN
                                                                                                                                                                            STANDARD;
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G_PROTEIN_RECEP_F1_2; 1.
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CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (P
79B9821C10841114 CRC64;
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EXTRACELLULAR (POTENTIAL)
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7 (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
                                                                                     Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                            PRT;
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; Murinae; Mus
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Pfam; PF00001;
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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YFLMSSNIRKIMCQLL
                                                YFFLCKSFRNSLISML
                                                                                                                                                          VFIIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFI
                                                                                                                                                                                                                   RHNAKGEAIFNFVLVVMFWLIFLLIILSYIKIGKNLLRISKRRSKFPNSGKYATTARN--
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
PS50262; G_PROTEIN_RECEP_F1_2; Transmembrane; G:
; G-protein coupled receptor; Transmembrane; G:
EXTRACELLULAR (POTENTIAL)
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0001; 7tm_1; 1.
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Pred. No. 4.9e
52; Mismatches
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4 (POTENTIAL).
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y. Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J. Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A., "NEDO human cDNA sequencing project.", "NEDO human cDNA sequencing project.", Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meindl A., Pusch C.M.;
"Physical mapping and exclusion of GPR
congenital stationary night blindness
Hum. Genet. 107:89-91(2000).
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                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99156852; pubMed-10036181;
Marchese A., Sawzdargo M., Nguyen T., Cheng R., Her
Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
"Discovery of three novel orphan G-protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schoneberg T., Schulz
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Mammalia; Eutheria;
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SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
TISSUE SPECIFICITY: BROADLY EXPRESSED.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                           300241;
PF00001; 7tm_1; 1.
S; PR00237; GPCRRHODOPSN
TE; PS00237; G_PROTEIN_R;
                                                                                                                                    BC020678;
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                                                                                                                                                           AK027780;
                                                                                                                                                                                    AF118670;
                                                                                                         HGNC:4490; GPR34
                                                                                                                                                                                                                                        d and this statement is not removes requires a license agreement (S) an email to license@isb-sib.ch).
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G_PROTEIN_RECEP_F1_1;
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  Ye R.D., Prossnitz E.R., Zou "Characterization of a human
          SEQUENCE FROM N.A.
MEDLINE=92028922; PubMed=1656963;
Ye R.D., Prossnitz E.R., Zou A.,
                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                 SFIVLIIFTICFVPYHAFRFIYISSQL-NVSSCYWKEIVHKTNEIMLVLSSFNSCLDPVM
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annotation
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6 (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR
3 (POTENTIAL).
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Pred. No. 6.8e-21;
3; Mismatches 152;
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5 (POTENTIAL)
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Chase P.B., Halonen M., Regan J.W.;

"Cloning of a human platelet-activating factor receptor gene:
evidence for an intron in the 5'-untranslated region.";
Am. J. Respit. Cell Mol. Biol. 8:240-244(1993).

-I- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Biochem.
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EMBL;
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EMBL;
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Seyfited C.E., Schweickart V.L., Godis
"The human platelet-activating factor
no introns and maps to chromosome 1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and characterization of the platelet-activating factor receptor gene expressed in the human heart."; Blochem. Biophys. Res. Commun. 189:617-624(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurachi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93112021;
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                                                M80436; AAA60001.1;

M76674; AAA60002.1;

D10202; BAA01050.1;

M88177; AAA60214.1;

M88177; AAA60214.1;

S52624; AAB24695.2;

L07334; AAA60108.1;

S56396; AAB25755.1;
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Gerard N.P., Gerard C.;
an leukocyte platelat-activating factor receptor. cDNA
cell surface expression, and construction of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     My Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M., Seyama Y., Matsumoto T., Noma M., Shimizu T.; ar cloning and expression of platelet-activating factor from human leukocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM
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Biophys. Res. C
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A40191.
A41079.
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(XX-1992) to
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Commun. 180:105-111(1991).
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EMBL/GenBank/DDBJ databases
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receptor gene (PTAFR) contains
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33555

PAFR_CAVPO P21556; 01-MAY-1991 01-AUG-1991 01-OCT-1996

(Rel. 18, Created)
(Rel. 19, Last sequence up
(Rel. 34, Last annotation

update)

STANDARD;

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Pfam; PF00001; 7tm_1; 1.
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                                                                                                                   SEFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVF 239
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32.6%;
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F -> L (IN REF. 6).
C -> R (IN REF. 6).
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KR -> TT (IN REF. 6).
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N_RECEP_F1_2; 1.
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1; Mismatches
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HOnda Z.-T., Nakamura M., Miki I., Minami M., Watanabe T., Sey
Okado H., Toh H., Ito K., Miyamoto T., Shimizu T.;
"Cloning by functional expression of platelet-activating facto
receptor from guinea-pig lung.";
Nature 349:342-346(1991).
-1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMO
PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY,
MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIA
ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITY
CALCIUM SECOND MESSENGER SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bloinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet PTAFR.
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                                                                                                                                                                                                                                                                                                                                G-protein coupled
                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
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 NLLGAKILSVVIW-----AFMFLLSLPNMILITNRQPRDKNVKKCSFLKSEFG---
                                                                         FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK
                                                                DSEFRYTLFPIVYSIIFVLGIIANGYVLWVFARLYPSKKLNEIKIFMVNLTVADLLFLIT
                            LPLWIVYYSNOGNWELPKELCNLAGCLEFINTYCSVAELGVITYNREQAVKYPIKTAQAT
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                                                                                                                                          38984 MW;
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30.7%;
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Pred.
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-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-93188173; PubMed-8383;
Birkenbach M.P., Josefsen K.,
                                                                                                                                                    TRANSMEM
                                                                                                                                                                                              PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                          Pfam; PF00001; 7tm_1;
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                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Epstein-Barr virus-induced genes: first protein-coupled peptide receptors.";
J. Virol. 67:2209-2220(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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Sus scrofa (Pig).
Eukaryota; Metazoa; (Mammalia; Eutheria; (Mammalia)
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15-JUN-2002 (Rel. 41, L
15-JUN-2002 (Rel. 41, L
Cysteinyl leukotriene r
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DISULFID
SEQUENCE
                                                                                                                                                                           Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).

-I- SUBCELLULAR LOCATION: Integral membrane protein.
-I- SUMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Q95N03;
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                                                                                                                                                                                                                                                                                                                       Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of the cloned rat and porcine cyste: receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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BY SIMILARITY.
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4; Mismatches
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7 (POTENTIAL).
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r 2 (CysLTR2).
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                          (See http://www.isb-sib.ch/announce/
                                                                  There are no restrictions on ong as its content is in no
                                                                                                                                                                                                                                                                                                                                               porcine cysteinyl leukotriene
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Best Local S
Matches 93
                              Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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15-JUL-1998 (Rel. 36, Last ann
Platelet activating factor rec
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                                                                                                                                                                                                          STANDARD;
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Rodentia;
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CYTOPLASMIC ()
6 (POTENTIAL)
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Pred. No. 4.4e-18;
2; Mismatches 134
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EXTRACELLULAR (POTENTIAL).
                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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lon update)
(PAF-R).
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Query Match
Best Local S
Matches 96
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DISULFID
SEQUENCE
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MGD; MGI:106066; Ptafr.
Interpro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.

1- SUBCELLULAR LOCATION: Integral membrane protein.

1- SIMILARITY: BELLONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T. Noma M., Shinizu T.;
Noma M., Shinizu T.;
"A murine platelet-activating factor receptor gene: cloning, chromosomal localization and up-regulation of expression by lipopolysaccharide in peritoneal resident macrophages.", Biochem. J. 314:671-678(1996)

1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemotaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96239129; PubMed=8670084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                          137
248 CEVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRN
                                                                                                                                                                                                                                    77
                                                                                                                                                                                                                                                                    70
                                                                  IVNYICQVIFWINFLI-VIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFI 247
                                      FIAFCFFLVFFLIFYCNLVIIHTLLTQPMRQQ--RKAGV----KRRALWMVCTVLAVFII 243
                                                                                                                TRKRGISLSLIIWVSIVATASYFLATDSTNLVPNKDGSGNITRCFEHYEPYSVPILVVHV 189
                                                                                                                                                      NLLGAKILSVVIWAFM-----FLLSLPNMILTNRQPRDKNVKKCSFLKSEFG---LVWHE
                                                                                                                                                                                                                  FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                          LPLWIVYYYNEGDWILPNFLCNVAGCLFFINTYCSVAFLGVITYNRYQAVAYPIKTAQAT 129
                                                                                                                                                                                                                                                                                                                                                      l Similarity
96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                               341 AA;
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y., Nakamura M., Waga I., Kume K., Izumi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39148 MW;
                                                                                                                                                                                                                                                                                                                                                                       20.6%;
29.9%;
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                                                                                                                                                                                                                                                                                                                                              Score 366; DB 1; Length 341; Pred. No. 5e-1B; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               7 (POTENTIAL).
CYTOPLASMIC (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
BY SIMILARITY.
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EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).
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7 (POTENTIAL).
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6 (POTENTIAL
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5 (POTENTIAL).
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4 (POTENTIAL).
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Search completed: December Job time : 35 secs 6, 2002, 10:04:55

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1: sp_archea:*
2: sp_bacteria
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4: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
12: sp_virus:*
13: sp_verteb:
13: sp_virus:*
14: sp_urclass
15: sp_varcheap
17: sp_archeap
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Match Length
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1778
1 MQAVDNLTSAPGNTSLCTRD......SQDNRKKEQDGGDPNEETPM 342
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Gapop 10.0 , Gapext 0.5
   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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sp_organelle:*
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    4 QBPV8
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Q9bbv8 homo sapien
Q8tdu7 homo sapien
Q9d812 mus musculu
Q96318 homo sapien
Q9by21 homo sapien
Q9by21 homo sapien
Q9by21 homo sapien
Q9be53 macaca fasc
Q9bxC2 homo sapien
Q9by61 homo sapien
Q9ty15 bos taurus
Q9by61 capra hircu
Q9try6 canis famil
Q9x8d4 sus scrofa
O57466 meleagris g
Q9pvy7 angullla an
Q9n0ul ovis aries
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304.5 304.5 304.5 301.5 301.5 301.5 301.5 29.5 29.5 29.5 29.5 29.5 29.5 29.5 29	336 322 321 318.5 318 314 314 309 309 309 304.5
17.1 17.1 17.1 17.1 17.1 16.9 16.8 16.8 16.7 16.5 16.5	18.9 18.1 18.1 17.9 17.9 17.4 17.4 17.4 17.4 17.1
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Q9r119 mus musculu Q8v169 mus musculu Q9v101 mus musculu Q9r0d1 mus musculu Q9f191 mus musculu Q9f191 mus musculu Q9g140 carassius a Q9g40 carassius a Q9g40 cercopithec Q9yc3 xenopus lae Q9tu47 cercopithec Q9tu47 cercopithec Q8vhp3 cavia porce Q9tu43 carcia porce Q9tu43 cercopithec Q9tu43 cercopithec Q9f120 rattus sp. Q9tu43 cercopithec Q9f120 rattus norv Q9tsn3 macaca fasc	mus cavi pan t mus homo macac acip homo meri mus mus mus

ALIGNMENTS

RT "Discovery and mapping of	RA Lewis T., Evans J.F., G			RP SECTENCE FROM N. A.		the	RT "An expressed sequence :		RX MEDLINE-21172992; PubMed-11273702;			protein-coupled red	RT "Molecular cloning of F	Wang V Cong	TISSUE-HEART:		NCBI_TaxID=9606;	Mammalia; Eutheria;		Homo sapiens (H	GPR86).	DE GPR86) (G protein-coupled		DT 01-JUN-2002 (TremBirel, 21,	01 - WIN - 2001	DT 01-JIN-2001 (Trawaire)	OGBOVS:	ID OGBDVB PREITMINARY:	RESULT 1	
of ten novel G protein-coupled receptor	Owd B.F.;	ich K.R., Cheng R., Vanti W.B., Arkhitko O.,	1-11574155;		13(2001).		expressed sequence tag (est) data mining strategy succeeding in	er H.C., Hellebrand S.;	1-11273702;		the EMBL/GenBank/DDBJ databases.	", a moter dene emecaring a pacacite	novel dene encoding a					Catarrhini: Hominidae:	Chordata; Craniata; Vertebrata; Euteleostomi;			GPR86) (G protein-coupled receptor) (G protein-coupled receptor	22.5	1), Last annotation undate)				PRT: 333 AA		

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Matches 154
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Best Local
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Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of a Novel Human ADP Recept J. Biol. Chem. 276:41479-41485(2001).

EMBL; AF345565; AAK29068.1; -.

EMBL; AF295368; AAK201664.1; -.

EMBL; AF411113; AAL26484.1; -.

EMBL; AF406692; AAL01038.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PRINTS; PR01655; UDPGLUCOSER.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UPPROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                    Takeda S., Kadowaki
"Identification of G
genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Putative G-protein coupled J
                                                                                                                              EMBL; AB083597; BAB89310.1;
                                                                                                                                                  Submitted
                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TDU7;
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                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11546776;
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55; Conservative
                        Similarity
                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                  (APR-2002) to the
                                                                                     333
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    Conservative
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Primates;
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                                                                                                                                                                                            S., Haga T., Taki
protein-coupled
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                   46.3%;
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                                                                                     WW.
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    57;
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                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                EMBL/GenBank/DDBJ
                   Score 823;
Pred. No. 2
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Pred. No. 7e-66;
7; Mismatches 102;
                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
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  Mismatches
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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A King B., Kochiwa H.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Szuki R., Tomita M., Wagner L., Washio T.,
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A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Geriboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Wyoshaw Boris A., Kangwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
EMBL; AK008013; BALLETTE
MGD: MGI:1921441; Gpr86.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; Tom_1; 1.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01655; UDPGLUCOSER.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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Q9D812;
01-JUN-2001 (TIEMBLEGL 17, C
01-JUN-2002 (TIEMBLEGL 17, L
01-JUN-2002 (TIEMBLEGL 21, L
2010001L106Rik protein.
GPR86 OR 2010001L06RIK.
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STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001).
EMBL; AK008013; BAB25409.1; -.
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Mammalia; Eutheria;
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LPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRNIFLK 134
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                                                                                                                                                                                                                                             Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosolri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Yinomiya K., Iwayanagi T.; "NEDO human cDNA sequencing project."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK027784; BAB55366.1; -. InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                        PRINTS; PRO1569; PZY12PRNCPTR.
PRINTS; PRO1655; UDPGLUCOSER.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TYEMBLIFEL. 19, Created)
01-DEC-2001 (TYEMBLIFEL. 19, Last sequence update)
01-JUN-2002 (TYEMBLIFEL. 21, Last annotation update)
CDNA FLJ14878 fls, Clone PLACE1003238, weakly similar to
protein-coupled receptor.
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                                           KFTQKVPCVRWGKARTAGSSEDHHSSQTD
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NTVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQ
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                                                                                                                                                                                                                                     PF00001; 7tm_1;
                                                                                                      al Similarity
140; Conser
                                                                                                   39.3%;
illarity 42.6%;
Conservative 6
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                                                                                                     Score 699.5;
Pred. No. 2.4e
7; Mismatches
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Pred. No. 9.1e-63;
3; Mismatches 111,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332
                                                                                                                    .4e-54;
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                                                                                                                                DB 4;
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Q9BY21;
01-JUN-2001 (Tremblrel. 1
01-JUN-2001 (Tremblrel. 1
01-JUN-2002 (Tremblrel. 2
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SEQUENCE FROM N.A.
MEDLINE=21458557; PubMed=11574155;
MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01655; UDPGLUCOSER.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Tr.
G-protein coupled receptor; Glycoprotein; Receptor; Tr.
SEQUENCE 358 AA; 41435 MW; FDF157295BE5D10F CRC64;
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[2]
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GPR87 OR
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MEDLINB-21172992; PubMed-11273702;

Wittenberger T., Schaller H.C., Hellebrand S.;

"An expressed sequence tag (est) data mining strathe discovery of new g-protein coupled receptors
J. Mol. Biol. 307:799-813(2001).
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Mammalia; Eutheria;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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NTVISDLLMILTEPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISELGLITIDRYQ 124
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42.2%;
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17, Last sequence update)
21, Last annotation update)
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                                                                                                                                                                                                                                                                                                       Score 694.5; |
Pred. No. 6.8e
68; Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21172992; Pubmed-1107000; Mittenberger T., Schaller H.C., Hellebrand S.; Wittenberger T., Schaller H.C., Hellebrand S.; "An expressed sequence tag (est) data mining strategy succeeding in the discovery of new g-protein coupled receptors.";

J. Mol. Biol. 307:799-813(2001).

-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00237; GPCRHODOPSN.

PRINTS; PR01655; UDPGLUCOSER.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.

SEQUENCE 359 AA; 41462 MW; 2EB313C273EFCDEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1934133; Gpr87.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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MEDLINE-21172992; PubMed-11273702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G-protein coupled
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TCFLPYHLCRIPFTFSNLDRLLDESAHKILYYCKEMTLFLSACNVCLDPIIYFFMCKSFS
                                                                                                                            EIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRK-KVNVKVFIIIAVFF
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                                                                                                                                                                                                KPFGDSRMYSITFTKVLSVCVWVIMAILSLPNIILTNGQPTKENIHDCMKLKSPLGAKWH
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BLrel. 17, Last sequence update)
BLrel. 21, Last annotation update)
receptor GPR87.
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Pred. No. 4.3
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tches 120;
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98ESIAT

98ESIA

98ES
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AC OCC GN DT DT RN OCC OCC GN PROCES
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Best Local S
Matches 105
                                                                                                                                                                                                            QBXC2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
Putative G-protein-coupled receptor
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01-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osada N., Hida M., Kusuda J., Tanuma I
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
libraries.";
                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                               09вхс2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01655; UDPGLUCOSER.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 228 AA; 26356 MW; 47907F5DBEEDD22C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2001) to the EMBL/GenBank/DDBJ EMBL; AB055816; BAB39342.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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TISSUE=HEART;
                         SEQUENCE FROM
                                                                           NCBI_TaxID=9606;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLiel. 17,
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46.7%; Pred. No. 4.9e-42;
Live 40; Mismatches 78;
                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
receptor FKSG78 (G prote
                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                       Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Zhang W., Wan T., Cao X.;

*Molecular cloning of a probable G protein-couple for the complex of the c
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Best Local
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   Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative G protein-coupled receptor GPCR1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCKRHODOPSN.
PRINTS; PR01655; UDPGLUCOSER.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; SEQUENCE 269 AA; 31443 MW; 1E7D498EE20717F6 CRC6
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Pfam; PF00001; 7tm_1; 1.
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"Identification of
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Q9TTY5;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-2000) to the EMBL; AF187321; AAF01439.2; EMBL; AJ295321; CAC43290.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               He B., Tiemann U., Kanitz W. Schmidt P., "Molecular characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yang W.S., Diehl J.
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01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1559; DÜFFYANTIGEN. PRINTS; PRO0237; GPCRRHODOPSN. PROSITE; PS00237; G_PROTEIN_RE
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Pfam; PF00001; 7tm_1; 1.
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"Partial Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
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                                                                                                                                                                                                 RPFKTSNPKNLLGAKILSVVIW-----AFMFLLSLPNMILTNRQPR---DKNVKKCSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KETTLFLAATNICMDPLIYIFLCKKFTEKLPCMQ--GRKTTASSQENHSSQTD
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LKSEFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVK
                                          RPIKTAQATTRKRGILLSLIIWVSIVGAASYFFVLD----STNREPNKTGSANITRC-F
                                                                                                                       MADLLFLYTLPLWIYYYNQGDWILPKFLCNLAGCFFFINTYCSVAFLAVITYNRFQAVT
                                                                                                                                                             ISDLLMILTEPEKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTT 127
                                                                                                                                                                                                                                                                                       101;
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                                                                                                                                                                                                                                                                                                                                                                                                       G_PROTEIN_RECEP_F1_1; UNKNOWN_1
G_PROTEIN_RECEP_F1_2; 1.
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Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                 39691 MW;
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16,
21,
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                                                                                                                                                                                                                                                                                     63;
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33
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Pred. No. 2.8e-32;
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on update)
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Euteleostomi; Canis.

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RESULT 12
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Best Local S
Matches 102
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capra hircus (Goat). Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21, Platelet-activating factor r
         Q9TTY6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01559; DUFFYANTIGEN.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
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Pfam; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2000) to the EMBL/GenBank/DDBJ EMBL; AF302764; AAG39982.1; -.
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les 102; Conservative
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                                                                                                                                     LDPFTYFFLCKSFRNSLISML-----KCPNSATS
                                                                                                                                                                                                                                                                                                                                                 RPEKTSNPKNLLGAKILSVVIW-----AFMFLLSLPNMILTNRQPR---DKNVKKCSF
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       PRELIMINARY;
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Caprine Platelet-Activating
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Pred. No. 1.3e
66; Mismatches
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Best Local
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                                                                                                                                                                                    Q9XSD4 PRELIMINARY; PRT; 342 AA.
Q9XSD4;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Platelet-activating factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
SEQUENCE FROM N.A.

Diehl J.R., Murphy K.E., Roudebush W.E.;
"Porcine (Sus scrofa) platelet-activating factor receptor DNA.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF124054; AAD28739.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang W.S., Diehl J.R., Murphy K.E.;
"Darrial Sequence of Canine Platelet-Activating Factor Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09TTY6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Platelet-activating factor receptor (Fragment).
                                                                                                         NCBI_TaxID=9823;
                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-1999) to the EMBL/G
EMBL; AF186831; AAF01435.1; -
InterPro; IPR000276; GPCR.Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                    292
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                                                                                                                                                                                                                                                                                                                                                                                                                     FRNSL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPHHLVQLPWTLA-----ELGFQSSSFHQGINDAHQVTLCLLSTNCVLDPIIYCFLTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRKRGFLVSLVIWVAIVAAASYFFILDSTNVVPS--KSGSGNITRC-FEHYEKGSVPVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLLGAKILSVVIW-----AFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSEFRYTLFPIVYSIIFVLGVVANSYVLWVFACLYPSKKLNEIKIFMVNLTMADLLFLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPFHFARIPYTLSQTRDVFDCTAENTLFY-----VKESTLWLTSLNACLDPFIYFFLCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
296
296 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
296
33902 MW;
                                                                                                                               Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.7%;
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5,1: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.466; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 368.5; DB 6; Pred. No. 5.4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5494C0771C45E101 CRC64;
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Indels Length

25;

Gaps

7;

61

304

249

237

189

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Euteleostomi; Sus.

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RESULT 14

057466

ID 057466

AC 05746

AC 057
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       Query Match
Best Local S
Matches 96
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Best Local
                                                                                                                                        HSSP; P34996; 1DDD.
InterPro; IPRO00276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                             Mol. Pharmacol. 52:928-934(1997).
EMBL; AF031897; AAC60339.1; -.
HSSP; P34996; 1DDD.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98086419; PubMed-9415702;
Boyer J.L., Waldo G.L., Harden T.I
"Molecular cloning and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           057466
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PRINTS; PRO0237; G_PCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9103;
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Pfam; PF00001;
Local 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRKHLSEKFYSLRGSRKCSRVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRN-----SLISMLKCPNSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPHHIVQLPWTLA-----ELGFQSGNFHQAINDAHQITLCLLSTNCVLDPIIYCFLTKK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPFHFARIPYTLSQTRDVFDCTAENTLFY----VKESTLWLTSLNACLDPFIYFFLCKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLLGAKILSVVIW-----AFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGLVWHEI
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                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 AA;
                                                                                                    374
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                    AA,
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                                                                                                 42594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.5%;
    20.0%; Score 356; DB 13; 30.8%; Pred. No. 8.7e-24; Live 55; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        830EA7542B528DAC CRC64;
                                                                                                    849C465722BDD02B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       T.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                            of an
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                                                                                                                                               UNKNOWN_1.
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RESULT 15
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Matches 87
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Q9PVY7;
Q9PVY7;
Q1-MAY-2000 (TIEMBLITE1. 13, C
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Q1-MAY-2002 (TIEMBLITE1. 20, L
Angiotensin receptor.
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRTHODOPSN.

PROSITE; PS00237; GPCRTEIN_RECEP_F1_1; 1.

PROSITE; PS00240; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

G-PROTEASE; UNKNOWN_1.

G-PROTEASE; UNKNOWN_1.

G-PROTEASE; UNKNOWN_1.
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-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anguilla anguilla (European freshwater eel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutilopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: INTEGRAL M
-1- SIMILARITY: BELONGS TO FAMILY 1
EMBL; AJ005132; CAB40835.1; -
HSSP; P34996; 1DDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                   LIPVVYGCNEVIGIVGNSMVVAVIYCYMKLKTVAN--IFVLNLAVSDLTFLITLPMWATF
                                                                                                                                                                                                LFPLLYTVLFEVGLITNGLAMRI---FEQIRSKSNFIIFLKNTVISDLLMILTFPFKILS
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  LSVVIWAFMFLLSLPNM--
                                                       TAMGYNWPFGGFLCKASAGLTIFNLYTSIFFLTSLSIDRYLAIVHPVRSRQRRTVVYARI 145
                                                                                                            DAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKI 143
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                                                                                                                                                                                                                                                                                  87; Conserv
                                                                                                                                                                                                                                                                                  Conservative
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· ILTNRQPRDKNVKKCSFLKSEFGLVWHEIVNYICQV---
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1.2e-22;
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Search completed: December $\,$ 6, 2002, 10:07:59
Job time: 104 secs

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Scoring table:
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1643.899 Million cell updates/sec
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PID:g190698 NCBIP:109814)

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
281.5	282	282	282.5	284.5	290.5	291.5	292.5	295	296	296.5	297	297.5	297.5	298	298.5
15.8	15.9	15.9	15.9	16.0	16.3	16.4	16.5	16.6	16.6	16.7	16.7	16.7	16.7	16.8	16.8
353	355	352	352	333	352	373	362	380	380	420	380	360	359	380	365
N	2	N	N	N	N	N	2	N	2	N	N	2	2	N	N
S28787	JQ1231	A43113	G00048	I38974	A45747	A47556	S33733	JC2338	S36143	I51667	A55259	A53611	I51372	A48227	S68679
neuropeptide Y/pep	interleukin-8 rece	chemokine (C-C) re	fusin (LESTRA) - c	G protein-coupled	neuropeptide Y/pep	ATP receptor P2u -	G protein-coupled	kappa opioid recep	kappa opioid recep	thrombin receptor	kappa opioid recep	interleukin-8 rece	angiotensin II rec	kappa opioid recep	G protein-coupled

ALIGNMENTS

A; Molecule type: DNA
A; Residues: 1-226, 'Tgf', 229-342 <SEY>
A; Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1;
A; Note: sequence extracted from NCBI backbone (NCBIN:109813, R; Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993 A; Note: the authors translated the codon AAT for residue 316 R; SeyIried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W. Genomics 13, 832-834, 1992 A; Title: The human platelet-activating factor receptor gene (A; Reference number: A42831; MUID:92347886; PMID:1322356 A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976 R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y Blochem. Biophys. Res. Commun. 189, 617-624, 1992 A;Title: Molecular cloning and characterization of the platelet-activating factor rec A;Reference number: JC1359; MUID:93112021; PMID:1281995 A;Accession: JC1359 A;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A;Experimental source: granulocyte, cell line HL-60 all
R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.; Bito, H.;
J; Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating factor receptor from A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079 R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G. Biochem. Biophys. Res. Commun. 180, 105-11, 1991
A;Title: Characterization of a human cDNA that encodes a A;Reference number: JH0479; MUID:92028922; PMID:1656963 A;Accession: JH0479 C;Accession: A40191; JH0479; A41079; JC1359; A42831; I51 R;Kunz, D.; Gerard, N.P.; Gerard, C. J. Biol. Chem. 267, 9101-9106, 11992 A;Title: The human leukocyte platelet-activating factor A;Reference number: A40191; MUID:92250505; PMID:1374385 A;Accession: A40191 platelet-activating factor receptor - human C;Species: Homo sapiens (man) C;Date: 28-Aug-1992 *sequence_revision 28-Aug-1992 *text_change C;Accession: A40191; JH0479; A41079; JC1359; A42831; I51923 A; Reference number: A; Accession: A42831 A; Molecule type: mRNA
A; Residues: 1-315,'N',317-342 <SUG> A; Molecule type: mRNA A; Residues: 1-342 <YER> A; Cross-references: A; Molecule type: mRNA A; Residues: 1-342 <KUN> A;Molecule type: mRNA A;Residues: 1-342 <NAK> A; Experimental source: heart A;Status: not compared with conceptual translation GB:M76674; NID:g456293; PIDN:AAA60002.1; receptor. functional receptor (PTAFR) contains no as Lys PID:g456294 20-Jun-2000 cDNA cloning, cell for intro plat

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A;Title: Cloning of A;Reference number A;Reference number A;Accession: I519;A;Accession: I519;A;Status: prelimit A;Molecule type: I
                                                                                                                                                                                                        platelet-activating factor receptor - guinea pig (; Species: Cavia porcellus (guinea pig) c; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change C; Accession: S13638 R; Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Se Nature 349, 342-345, 1991 A; Title: Cloning by functional expression of platelet-activating A; Reference number: S13638; MUID:91101726; PMID:1846231
                                                                                                                                                                                                                                                                                                                                         RESULT
S13638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:128806; OMIM:173393
A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane
E;17-38/Domain: transmembrane #status predicted <TRI>
F;54-75/Domain: transmembrane #status predicted <TII>
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                                                                                                   CPP
                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-342 <HON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: PTAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;17-38/Domain: transmembrane #status predicted <TRI>;54-75/Domain: transmembrane #status predicted <TII>;92-113/Domain: transmembrane #status predicted <III>;114-155/Domain: transmembrane #status predicted <TIV>;184-205/Domain: transmembrane #status predicted <TRV>;233-253/Domain: transmembrane #status predicted <TVI>
                                                                                               ;Cross-references: GB:X56736; NII;
;Note: the species of guinea pig
;Superfamily: ATP receptor P2u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,ille: Cloning of a human platelet-activating factor receptor gene: evidence;Reference number: I51923; MUID:93192035; PMID:8383507; RACCESSION: I51923
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                                                                  Query Match
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Best Local Similarity
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 DYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLLMILT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPFKTSNPKNLLGAKILSVVIW-----AFMFLLSLPNMILTNRQPRDK----NVKKCSFLK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTT
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                                    Conservative
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                                                                                                              NID:g49442; PIDN:CAA40060.1; PID:g49443 pig is not identified; in GenBank entry
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Pred. No. 1
                                  Pred. No. 2.1e
6; Mismatches
                                                 Score 392.5; DB 2; Pred. No. 2.1e-26;
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.5e-26;
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T Virol. 67, 2209-2220,
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A; Residues: 1-361 <BIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127096,
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane proteir
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A;Title: Epstein-Barr virus-induced genes:
A;Reference number: A45680; MUID:93188173;
A;Accession: B45680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G protein-coupled peptide receptor EBI 2 - human C:Species: Homo sapiens (man) C:Date: 21-Sep-193 #sequence_revision 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MQAVDNLT----SAPGNTSLCTRDYKITQVLEPLLYTVLFFVGLITNGLAMRIFFQIRSK
FTVCLMNFNCCMDPFIYFFACKGYKRKVMRMLK-RQVSVSISSAVKSAPEENSREMTETQ
                                 STLWLTSLNACLDPFIYFFLCKSFRNSLISMLKCPNSATSLSQDNRKKEQDGGDPNEETP
                                                                                                          SGVNK----KALNT-IILIIVVFVLCFTPYHVAIIQHMIKKLRFSNFLECSQRHSFQISLH
                                                                                                                                                                                                                  RITCMEYPNFEETKSLPW---ILLGACFIGYVLPLIIILICYSQICCKLFRTAKQNPLTEK
                                                                                                                                                                                                                                                                        DKNVKKCSFLKSEFGLVWHEIVNYICQVIFWINFLIVIVCYTLITKELYRS----YVRT
                                                                                                                                                                                                                                                                                                                             GVNFMTCLSIDRFIAVVHPLRYNKIKRIEHAKGVCIFVWILVFAQTLPLLINPMSKQEAE
                                                                                                                                                                                                                                                                                                                                                                             SISFIGLITIDRYQKTTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMI--LTNRQPR 168
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                                                                                                                                                             RGVGKVPRKKVNVKVFIIIAVFFICFVPFHFARIPYTLSQTR--DVFDCTAENTLFYVKE
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Pred. No. 2.9e-25;
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PMID:8383238
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platelet-activating factor receptor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text C;Accession: S43252 R;Bito, H.; Honda, Z.; Nakamura, M.; Shimizu, T. Risto, H.; Honda, Z.; Nakamura, M.; Shimizu, T. Risto, H.; Biochem. 221, 211-218, 1994 A;Title: Cloning, expression and tissue distribution of A;Reference number: S43252; MUID:94222063; PMID:8168510 A;Accession: S43252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     platelet activating factor receptor - mouse (;Species: Mus musculus (house mouse) C;Date: 28 -Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000 C;Accession: $63666 R;Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimi Blochem. J. 314, 671-678, 1996 Blochem. J. 314, 671-678, 1996 A;Reference number: $63666; MUID:96239129; PMID:8670084 A;Accession: $63666
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A; Residues: 1-341 <BIT>
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A; Residues: 1-341 <ISH>
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                                     DYKITQVLFPLLYTVLFFVGLITNGLAMRIF---FQIRSKSNFIIFLKNTVISDLLMILT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLLGAKILSVVIWAFM-----FLLSLPNMILTNRQPRDKNVKKCSFLKSEFG---LVWHE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPLWIVYYYNEGDWILPNELCNVAGCLFFINTYCSVAFLGVITYNRYQAVAYPIKTAQAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYKITQVLFPLLYTVLFFVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLLMILT 76
   HLSEKFYSMRSSRKC-SRATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIAFCFFLVFFLIFYCNLVIIHTLLTQPMRQQ--RKAGV----KRRALWMVCTVLAVFII 243
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                                                                         Score 362; DB Pred. No. 8.9e 56; Mismatches
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SNPKNLLGAKILSVVIWAFMFLLSLPNMIL--TNRQPRDKNVKKC--SFLKSEFGLVWHE 188

 14 TSLCTRDYKITQVLFPLLYTVLFFVGLITNGLAMRIF-FQIRSKSNFIIFLKNTVISDLL 72

SSNCSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLL 62

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F;89-109/Domain: transmembrane #status predicted <TM3>F;133-153/Domain: transmembrane #status predicted <TM4>F;133-150/Domain: transmembrane #status predicted <TM5>F;277-248/Domain: transmembrane #status predicted <TM5>F;269-292/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                 C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TMA>
F;51-74/Domain: transmembrane #status predicted <TMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A. Biochem. Biophys. Res. Commun. 219, 105-110, 1996 A;Title: Identification of 6H1 as a P2V purinoceptor: P2Y5. A;Reference number: JC4618; MUID:96190677; PMID:8619790 A;Accession: JC4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Kaplan, M.H.; Smith, D.I.; St
T Tmmunol. 151, 628-636, 1993
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N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change
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A; Residues: 1-308 <WEB>
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                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: T-cells
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     l Similarity
87; Conserv
     Conservative
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  20.1%; Score 357.5; DB 2; 29.5%; Pred. No. 1.9e-23; ative 68; Mismatches 125;
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Intro 17 purinergic receptor P2Y5 - human N;Alternate names: G-protein coupled receptor C;Species: Homo sapiens (man) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #t C;Accession: T09508 R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Pay submitted to the EMBL Data Library, April 1997 A;Description: The human purinergic receptor P2Y5 is A;Reference number: Z16705 A;Reference number: Z16705 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-344 <BOH>
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C; Species: Bos primi
C; Date: 19-Mar-1997 i
C; Accession: S15403
R; Sasaki, K.; Yamano
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A;Residues: 1-359 <SAS>
A;Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
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A;Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiot. A;Reference number: S15403; MUID:91251900; PMID:2041569
A;Accession: S15403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 95; Conserv
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                                                                                                                                                                                                                                             FLQLLKYIPPKAKSHSNLSTKMSTLSYRPSENGNSSTKKP
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                                                                                                                                                                                                                                                                                                                                                                           SVVIWAFMFLLSLPNMILTN-RQPRDKNVKKCSF-----LKSEFGLVWHEIVNYICQ 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKLGTGPLRTEVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVPYNITLILYSLMRTQTWINCSVVTAVRTMYPV---TLCIAVSNCCFDPIVYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVPFHFARIPYTLSQTRDVFDC---TAENTLFYVKESTLWLTSLNACLDPFIYFF
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30-233, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 339; DB 2
Pred. No. 9e-22;
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                              GB/EMBL/DDBJ
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angiotensin II receptor type 1b c;Species: Homo sapiens (man) C;Date: 29-May-198 #sequence_re C;Accession: I39418
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C; Superfamily: ATP receptor P2u
C; Keywords: G protein-coupled r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-359 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 199, 467-474, 1994
A; Title: Novel subtype of human angiotensin II type 1 receptor:
A; Reference number: 139418; MUID:94183213; PMID:8135787
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: I39418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: vertebrate rhodopsin
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Best Local
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                                                                                VIFWINFLIVIVCYTLITKELYRSYVRTRGVGKVPRKKVNVKVFIIIAVFFICFVPFHFA 255
                                                                                                                                    CITIWLLAGLASLPATIHRNVFFIENTNITVCAFHYESRNSTLPIGLGLTKNILGS--C-
                                                                                                                                                                                 SVVIWAFMFLLSLPNMILIN-RQPRDKNVKKCSF-----LKSEFGLVWHEIVNYICQ 195
                                                                                                                                                                                                                              AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKSRLRRTMLVAKVT
                                                                                                                                                                                                                                                                        AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                       VMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FVPFHFARIPYTLSQTRDVFDCT---AENTLFYVKESTLWLTSLNACLDPFIYFFLCKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKTLRTKRNAKIVCTGVWLTVIGGSAPAVFVQSTHSQGNNASEACFENFPEATWKTYLSR
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                                                 ----FPFLIILTSYTLIWKALKKAYEIQK---NNPRNDDIFRIIMAIVLFFF-
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Pred. No. 1.1e-21;
9; Mismatches 146
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 329; DB 2;
Pred. No. 6.6e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 137;
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proteinase activated receptor 2 - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999 C;Accession: I48705 R.Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J. J. Biol. Chem. 270, 5950-5955, 1995 A;Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular A;Reference number: I48705; MUID:95197620; PMID:7890726 A;Accession: I48705 MUID:95197620; PMID:7890726 A;Accession: I48705 MUID:95197620; PMID:7890726 A;Accession: I48705 Translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-399 <RES> A;Cross-references: EMBL:Z48043; NID:g663020; PIDN:CAA88097.1; PID:g663021 C;Superfamily: ATP receptor P2u
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$44425
$C.; Species: Canis lupus familiaris (dog)
$C.; Species: Canis lupus familiaris (dog)
$C.; Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
$C.; Accession: $44425
$C.; Accession: $44425
$R.; Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
$FEBS Lett. 343, 146-150, 1994
                                                                                                                                                                                                                                                      RESULT
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A;Experimental source: liver
C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Molecular cloning of the canine an A;Reference number: S44425; MUID:94222188; A;Accession: S44425
A;Status: nucleic acid sequence not shown
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A; Residues: 1-359 <BUR>
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   Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITIWLLAGLASLPTIIHRNVFFIENTNITVCAFHYESQNSTLPIGLGLT-KNILGFL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT 88
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                                                                                                                                                                                                                                                                                                                                                                                                           ARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISMLK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYVAIVHPMKSPVRRTMLMAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          -FPFLIILTSYTLIWKTLKRAYEIQK---NKPRNDDIFKIIMAIVLFFFFSWVPHQI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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    18.3%;
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Pred. No. 1.2e-
54; Mismatches
    Score
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A;Experimental source: proximal tubule cells A;Note: sequence extracted from NCBI backbone (NCBIN:129600, | C;Superiamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A;Title: Cloning of a rabbit kidney cortex
A;Reference number: A48857; MUID:93236091;
A;Accession: A48857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiotensin II receptor type 1 - rabbit
C;Species: oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Dec:1993 #sequence_revision 18-Nov-1994
C;Accession: A48857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-359 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:S59041; NID:g299614; PIDN:AAB26239.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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Matches 92; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 VLEPLLYTVLEEVGLITNGLA-MRIFFQIRSKSNFIIFLKNTVISDLLMILTEPEKILSD 84
                                                                                                                                                                                                                                                              SVVIWAEMFLLSLPNMILTN-RQPRDKNVKKCSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCRSVRTVNRMQISLS-SNKFSRKSGSYSSSST
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                                                                                                                                                                                                               CIIIWLLAGLASLPAIIHRNVFFIENTNITVCAFHYESQNSTLPIGLGLT-KNILGFL--
                                                                                                                                                                                                                                                                                                                                                                  AKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQKTTRPFKTSNPKNLLGAKIL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLVVHYFLIKTQ-----RQSHVYALYLVALCLSTLNSCIDPFVYYFVSKDFRDHARNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAVGVSLAIWLLIFLVTIPLYVMKQTIYIPA-LNITTCHDVLPEEVLV-GDMFNYFLSLA
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FTFLDVLIQLGVIHDCRIADIVDTAMPITICIAYFNNCLNPLFYGFLGKKFKKYFLQLLK 318
                                                                                                                                                                                                                                                                                                                     AMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSIDRYLAIVHPMKSRLRRTMLVAKVT 148
                                                                                                                                                                                                                                                                                                                                                                                                                            VMIPTLYSIIFVVGIFGNSLAVIVIYFYMKLKTVASVFLLNLALADLCFLLTLPLWAVYT 88
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                                                 ARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFRNSLISMLK 314
                                                                                                      ----FPFLIILTSYTLIWKALKKAYEIQK---NKPRNDDIFKIIMAIVLFFFFSWVPHQI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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Pred. No. 1.5e-20;
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                                                                                                                                                                                                                                                              -LKSEFGLVWHEIVNYICQ 195
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319 YIPPKAKSHSNLSTK 333

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N;Alternate names: angiotensin II receptor 1A C:Species: Homo sapiens (man) C:Decies: Homo sapiens (man) C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #sequence_revision 09-Oct-1992 #sequence_revision 09-Oct-1992 #sequence_revision 09-Oct-1992 #sequence_revision 09-Oct-1992 #sequence_revision 09-Oct-1992 C:Accession: JC1104; JQ1402; JH0574; JH0267; A44014; S18983 R:Mauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z. Biochem. Biophys. Res. Commun. 186, 277-284, 1992 A;Title: Cloning, expression, and characterization of a gene enc. A.Reference number: JC1104; MUID:92337608; PMID:1378723 A;Accession: JC1104
                                                                                                                                                                                                                                                                                                       A;Gene: GDB:AGTR1

A;Cross-references: GDB:132359; OMIM:106165

A;Map position: 3q21-3q25

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane

F;30-53/Domain: transmembrane #status predicted <TMN2>

F;55-90/Domain: transmembrane #status predicted <TMN2>
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R;Furuta, H.; Guo, D.F.; Inagami, T.
R;Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Blophys. Res. Commun. 183, 8-13, 1992
A;Title: Molecular cloning and sequencing of the gene encoding human angiotensin A;Reference number: JQ1402; MUID:92181475; PMID:1543512
A;Accession: JQ1402
                                                                                                                                                      F;103-124/Domain: transmembrane #status predicted <TM3>
F;145-167/Domain: transmembrane #status predicted <TM4>
F;145-104-216/Domain: transmembrane #status predicted <TM5>
F;194-216/Domain: transmembrane #status predicted <TM5>
F;241-264/Domain: transmembrane #status predicted <TM6>
F;281-305/Domain: transmembrane #status predicted <TM7>
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A;Experimental source: liver
R;Takayanagi, R; Ohnaka, K; Sakai, Y; Nakao, R; Yanase, T.; Haji, M.; Inagami, T.;
Biochem. Biophys. Res. Commun. 183, 910-916, 1992
Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A;Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human A;Reference number: JH0267; MUID:92198490; PMID:1550596
A;Accession: JH0267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: lymphocyte R; Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten R; Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten Biochem. Blophys. Res. Commun. 183, 989-995, 1992
A; Title: Cloning and characterization of a human angiotensin II A; Reference number: JH0574; MUID:92231907; PMID:1567413
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A;Residues: 1-359 <CUR>
A;Cross-references: GB:M93394; NID:9178680; PID:9178681
A;Note: sequence extracted from NCBI backbone (NCBIN:111831,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Curnow, K.M.; Pascoe, L.; White, P.C.
Mol. Endocrinol. 6, 1113-1118, 1992
A;Title: Genetic analysis of the human type-1 angiotensin A;Reference number: A44014; MUID:92375105; PMID:1508224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-359 < TA
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A; Residues: 1-359 <BER>
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A; Residues: 1-359 <F
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                                                                      Query Match
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                                        Local
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names: angiotensin II receptor
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28.7%;
                                                                                                                                      carbohydrate
      56;
      Pred. No. 3.2e-20;
5; Mismatches 139;
                                                            Score 321;
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                                                                   DB 2;
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angiotensin A42656 RESULT

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receptor type

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R; Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D. Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A; Title: Cloning of a human heptahelical receptor closely related A; Reference number: JC5549; MUID:97366805; PMID:9223435
A; Accession: JC5549
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C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 *sequence_revision 05-Sep-1997 *text_change 24-Sep-1999
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A; Residues: 1-370 < JAN>
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                                   295 PFIYFFLCKSFRNS 308
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                                                                         LKMITVHMAVFVVCFVPYNSVLFLYALVRSQAITNCFLERFAKIMYPITLCLATLNCCFD
                                                                                                       NVKVFIIIAVFFICFVPFHFARIPYTLSQTRDVFDCTAENTLFYVKESTLWLTSLNACLD
                                                                                                                                             KRVWKTYLSKITIFIEVVGFIIPLILNVSCSSVVLRTLRKPATLSQIGTN-----KKKV
                                                                                                                                                                               --VWHEIVNYICQVIFWINFLIVIV----CYTLITKELYR---
                                                                                                                                                                                                                   IVYPFRSRTIRTRNSAIVCAGVWILVLSGGISASLFST----TNVNNATTTCFE-GLS 193
                                                                                                                                                                                                                                                    TTRPFKTSNPKNLLGAKILSVVIWAFMFLLSLPNMILTNRQPRDKNVKKCSFLKSEFGL- 184
                                                                                                                                                                                                                                                                                                                            TVISDLLMILTFPFKILSDAKLGTGPLRTFVCQVTSVIFYFTMYISISFLGLITIDRYQK 125
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27.7%;
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Pred. No. 3.3e-20;
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N;Alternate names: angiotensin II receptor chain B
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A42656; s20423
R;Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A;Title: Cloning and expression of a novel angiotensin II receptor subtype.
A;Reference number: A42656; MUID:92250585; PMID:1374402
A;Accession: A42656
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A;Molecule type: mRNA
A;Rosidues: 1-359 <IWA>
A;Cross-references: GB:X64052; NID:g57521; PIDN:CAA45410.1; PID:g57522
C;Superfamily: vertebrate rhodopsin
Search completed: December Job time: 22 secs
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FEBS Lett. 298, 257-260, 1992
A;Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A;Reference number: S20423; MUID:92183879; PMID:1544458
A;Accession: S20423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBIP:100268) R;Iwai, N.; Inagami, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: G protein-coupled receptor; transmembrane protein
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A;Experimental source: adrenal cortex
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A; Residues: 1-359 <SAN>
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Matches 92
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                                                                                                316 LLKYIPPTAKS 326
                                                                                                                                                 312 MLK-CPNSATS 321
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                      2002, 10:05:23
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